



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 167604

TO: Catherine Joyce  
Location: REM/4C04/3C18  
Art Unit: 1642  
Tuesday, October 04, 2005

Case Serial Number: 10/645094

From: Edward Hart  
Location: Biotech-Chem Library  
REM-1A55  
Phone: 571-272-2512

[edward.hart@uspto.gov](mailto:edward.hart@uspto.gov)

### Search Notes

Examiner Joyce,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

**THIS PAGE BLANK (USPTO)**

STIC-Biotech/ChemLib

167604

From: Joyce, Catherine  
Sent: Monday, October 03, 2005 4:11 PM  
To: STIC-Biotech/ChemLib  
Subject: 10/645094

Please search the following sequences:

SEQ ID NO:1 (polypeptide)

Catherine Joyce  
Art Unit 1642  
Ph. 571-272-3321  
Office: 4C04  
Mailbox: 3C18

RECEIVED  
OCT -4 2005  
STIC-BIOTECH/ChemLib  
(STIC)

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: 10/4/05  
Date completed: 10/4/05  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search 1  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: DP  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

THIS PAGE BLANK (USPTO)

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

✓

**THIS PAGE BLANK (uspto)**

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpm

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapm

***Because they contain data that is confidential, the results of Pending database searches should not be left in the case.***

**THIS PAGE BLANK (USPTO)**



# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



**THIS PAGE BLANK (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 13:46:40 ; Search time 180 Seconds  
(without alignments)  
1490.719 Million cell updates/sec

Title: US-10-645-094-1

Perfect score: 2703

Sequence: 1 MNLHVWKLSVSVSLITLY.....TNINKVANEESTIETKDEL 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2699	99.9	524	Q918A7	Q918A7 scomber jap
2	1156.5	42.8	523	Q8VEN4	Q8VEN4 mus musculus
3	1096.5	40.6	504	Q90W54	Q90W54 agkistrodon
4	1089.5	40.3	504	Q6STF1	Q6STF1 agkistrodon
5	1079.5	39.9	516	1 OXLA AGKRH	P81382 agkistrodon
6	1063.5	39.3	516	2 Q9PWC9	Q9PWC9 crotalus at
7	1059.5	39.2	497	2 Q6TGO9	Q6TGO9 bothrops ja
8	1059.5	39.2	516	1 OXLA CROAD	Q93364 crotalus ad
9	1058.5	39.2	478	2 Q6TGO8	Q6TGO8 bothrops mo
10	1055.5	39.0	516	2 Q6WP39	Q6WP39 trimeresuru
11	1052.5	38.9	516	2 Q7T062	Q7T062 trimeresuru
12	1048.5	38.8	523	2 Q9UJK6	Q9UJK6 mus musculus
13	1034	38.3	630	1 FIG1 MOUSE	Q09046 mus musculus
14	1034	38.3	630	2 Q6YBV6	Q6YBV6 mus musculus
15	1034	38.3	630	2 Q6YDI8	Q6YDI8 mus musculus
16	1030	38.1	630	2 Q6Y632	Q6Y632 mus musculus
17	999	37.0	567	1 FIG1 HUMAN	Q96RQ9 homo sapien
18	999	37.0	588	2 Q8TEM5	Q8TEM5 homo sapien
19	999	37.0	588	2 Q6P2Q3	Q6P2Q3 homo sapien
20	823.5	30.5	490	2 Q739P2	Q739P2 bacillus ce
21	818.5	30.3	482	2 Q81EG3	Q81EG3 bacillus ce
22	818.5	30.3	485	2 Q31334	Q31334 bacillus ce
23	817.5	30.2	478	2 Q81RW3	Q81RW3 bacillus th
24	812.5	30.1	485	2 Q6HJU8	Q6HJU8 bacillus th
25	807.5	29.9	482	2 Q63CE2	Q63CE2 bacillus an
26	807.5	29.9	482	2 Q81RM4	Q81RM4 bacillus an
27	796.5	29.5	478	2 Q739X9	Q739X9 bacillus ce
28	777.5	28.8	478	2 Q63CN0	Q63CN0 bacillus ce
29	773.5	28.6	478	2 Q6HK30	Q6HK30 bacillus th
30	761.5	28.2	478	2 Q81EP3	Q81EP3 bacillus ce
31	751	27.8	509	2 Q8R2G8	Q8R2G8 mus musculus

RESULT 1

Q918A7

ID Q918A7 PRELIMINARY; PRT; 524 AA.

AC Q918A7; 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Endoplasmic reticulum lumenal L-amino acid oxidase precursor.

GN Name=lao;

OS Scomber japonicus (Chub mackerel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;

OC Scombridae; Scomber.

OX NCBI\_TaxID=13676;

RN [1]\_TaxID=13676;

RP SEQUENCE FROM N.A.

RX MEDLINE=20363838; PubMed=10903755;

RA Jung S.K., Mai A., Iwamoto M., Arizono N., Fujimoto D., Sakamaki K.,

RA Yonehara S.;

RT "Purification and cloning of an apoptosis-inducing protein derived

from fish infected with Anisakis simplex, a causative nematode of

human anisakiasis.;"

RL J. Immunol. 165:1491-1497(2000).

DR EMBL; AJ400871; CAC00499.1; -.

DR HSSP; P81382; 1F8S.

DR GO; GO:0016491; P:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000759; Adrnxd\_reductase.

DR InterPro; IPR001613; Amino oxidase.

DR InterPro; IPR002937; Amino oxidase.

DR InterPro; IPR000205; NAD BS.

DR Pfam; PF01593; Amino oxidase; 1.

DR PRINTS; PR00419; ADXRDTASE.

DR PRINTS; PR00757; AMINEOXDASEF.

DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.

KW Signal.

FT SIGNAL. 1 30 Potential.

FT CHAIN. 31 524 endoplasmic reticulum lumenal L-amino

acid oxidase.

SQ SEQUENCE 524 AA; 58623 MW; 5C17ACA07E74897E CRC64;

Query Match 99.9%; Score 2699; DB 2; Length 524;

Best Local Similarity 99.8%; Pred. No. 1.6e-156;

Matches 523; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNLHVWKLSVSVSLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNGLPHINTSH 60

Db 1 MNLHVWKLSVSVSLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNGLPHINTSH 60

OY 61 HWIVGAGMAGLTAALKLQDAGHTVTILEANDRVGRVETVNEKEGYAENGAMRIPSS 120

Db 61 HWIVGAGMAGLTAALKLQDAGHTVTILEANDRVGRVETVNEKEGYAENGAMRIPSS 120

QY	121	HRIVQWVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVQENPDVLYKYNVSESEKGISAD	180	DR	HSSP: P81382; 1F8R.
Db	121	HRIVQWVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVQENPDVLYKYNVSESEKGISAD	180	DR	MGD; MGI:2140628; Laol.
QY	181	DLLDRALQKVEEVANGCKAALKYDRYSVKYKLEGGISPGAVRMIGDOLLNEQSLMY	240	DR	GO; GO:0005615; C:extracellular space; TAS.
Db	181	DLLDRALQKVEEVANGCKAALKYDRYSVKYKLEGGISPGAVRMIGDOLLNEQSLMY	240	DR	GO; GO:0001716; F:L-amino-acid oxidase activity; IDA.
QY	241	TALSEMIYDQADVNDVSIVTHEYTGSDLLPEAFSLVDLPVILLNSKVKHIRQSDKGVIVS	300	DR	GO; GO:0009063; P:amino acid catabolism; IDA.
Db	241	TALSEMIYDQADVNDVSIVTHEYTGSDLLPEAFSLVDLPVILLNSKVKHIRQSDKGVIVS	300	DR	Pfam: PF01593; Amino oxidase; 1.
QY	301	YQTGNESLMDSADIVLVTAKAALFIDFPDPLSISKMEALRSVHSDSTKILLTPRD	360	DR	PRINTS; PR00419; ADXRDITASE.
Db	301	YQTGNESLMDSADIVLVTAKAALFIDFPDPLSISKMEALRSVHSDSTKILLTPRD	360	DR	PRINTS; PR00757; AMINOXIDASEF.
QY	361	KFEWDDGIRGKSIITDGPGRYIYPSHSPHTNETIGVLLASVTWSDSLLFLGASDEBLK	420	DR	PRINTS; PR0370; FMOXGENASE.
Db	361	KFEWDDGIRGKSIITDGPGRYIYPSHSPHTNETIGVLLASVTWSDSLLFLGASDEBLK	420	SQ	SEQUENCE 523 AA; 58028 MW; F6D31592D7117A0B CRC64;
QY	421	ELALRDLAKIHGEQVWDKCTGIVVKWSADPYSLGAPALFTPYOHLEYAQELFSSEGRVH	480		
Db	421	ELALRDLAKIHGEQVWDKCTGIVVKWSADPYSLGAPALFTPYOHLEYAQELFSSEGRVH	480		
QY	481	PAGEHTAFPHAWIETSMKSAIRAAATNINKVANEESTIEHTKDEL	524		
Db	481	PAGEHTAFPHAWIETSMKSAIRAAATNINKVANEESTIEHTKDEL	524		
RESULT 2					
ID	Q8VEN4	PRELIMINARY;	PRT; 523 AA.		
AC	Q8VEN4;				
DT	01-MAR-2002	(T:EMBLrel. 20, Created)			
DT	01-MAR-2002	(T:EMBLrel. 20, Last sequence update)			
DT	01-OCT-2003	(T:EMBLrel. 25, Last annotation update)			
DE	L-amino acid oxidase 1.				
GN	Name=Laol;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=FVB/N; TISSUE=Mammary tumor;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Vilaillon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Kryzysinski M.I., Skalska U., Smalusz D.E., Schnerch J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=FVB/N; TISSUE=Mammary tumor;				
RA	Strausberg R.;				
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC017599; AAH17599.1; -.				

DR	HSSP: P81382; 1F8R.
DR	MGD; MGI:2140628; Laol.
DR	GO; GO:0005615; C:extracellular space; TAS.
DR	GO; GO:0001716; F:L-amino-acid oxidase activity; IDA.
DR	GO; GO:0009063; P:amino acid catabolism; IDA.
DR	Pfam: PF01593; Amino oxidase; 1.
DR	PRINTS; PR00419; ADXRDITASE.
DR	PRINTS; PR00757; AMINEOXIDASEF.
DR	PRINTS; PR00370; FMOXYGENASE.
SQ	SEQUENCE 523 AA; 58028 MW; F6D31592D7117A0B CRC64;
Query Match 42.8%; Score 1156.5; DB 2; Length 523;	
Best Local Similarity 47.1%; Pred. No. 3.6e-63;	
Matches 235; Conservative 85; Mismatches 172; Indels 7; Gaps 4;	
QY	27 LSLKEHLADLCEDKDYDTLLQTLNGLPHINTSHHVIVVAGMAGLTAAKLLQDAGHTVT 86
Db	25 LALYENLVKCFQDPDEAFLLIAQNLHTSPLSKRVVVVAGWAGLVAAKTLQDAGHEVT 84
QY	87 ILEANDRVGGRVETRYNEKEGYAEMGAMRIPSSHRIVQWFKVLGVEMNEFVMTDDNTF 146
Db	85 ILEASNHIGGRVTVLRNKEEGWLELGPMPRIPESHKLIHTYVQKGLKLNKFNQYDSNTW 144
QY	147 YLVNGVREERTYVVOENPDVLYKYNVSESEKGISADDDLLDRALQKVEEVEANGCKAALEKY 206
Db	145 YLLNGQRYRASEVMANPGILGYPLRPEKNTVTDLFYQAITKIKPHRKTSSNCQLLSLY 204
QY	207 DRYSVKEYLKEEGGLSPGAVRMIGDGLNEOSLMYLTALSEMIYDQADVNDVSIVTHEVTGS 266
Db	205 DSYSTRAYLMKEGTLKSGALEMIGDINNENAGYKSLLESRLIASIFSKSDQFSEITGGF 264
QY	267 DLLPEAF-LSVLDVPILLNSKVKHIRQSDKGVIVSYQT-GNESLMPLDLSADIVLVTTAK 324
Db	265 DQPLNGLSASLKPCTIRLGSKVERVVRDGPVKVMYRTDGTPTSALHKLTAIYAIITASAK 324
QY	325 AALFIDPDPPLSISKMEALRSVHSDSTKILLTPRDKFEDDGGIRGCKSITDGPGRYIY 384
Db	325 ATRLITFPPLSREKTHALRSVHTSATKVLVNCERFWEQDGIIRGGYSITDRPSRFIY 384
QY	385 PSHSFHTNETIGVLLASVTWSDSLLFLGASDEBLKELALRDLAKIH---GEQVWDKCTG 441
Db	385 PSHSLPGKK--GVLLASFTVGDDSSFFAALKPNQVVDVLDLAAVHRIPKEELKRCMKPK 442
QY	442 VIVKWSADPYSLGAPALFTPYOHLEYAQELFSSEGRVHFAGEHTAFPHAWIETSMKSAI 501
Db	443 SAIKHWSLDPLTIGATTEFTPYQFVDYSKQLSQPEGRIFYAGEHTCLPHSWIDTAIKSGI 502
QY	502 RAATNINKVANEESTIHT 520
Db	503 RASCNIQAAVDKEATRIGHT 521
RESULT 3	
ID	Q90W54 PRELIMINARY; PRT; 504 AA.
AC	Q90W54;
DT	01-DEC-2001 (T:EMBLrel. 19, Created)
DT	01-DEC-2001 (T:EMBLrel. 19, Last sequence update)
DT	01-OCT-2003 (T:EMBLrel. 25, Last annotation update)
DE	M-LAO precursor (EC 1.4.3.2).
OS	Agkistrodon halsys blomhoffii (Mamushi) (Gloydius blomhoffii).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Viperidae; Crotalinae; Gloydius.
OX	NCBI_TaxID=242054;
RP	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Venom;
RX	MEDLINE=21240157; PubMed=11341935; DOI=10.1016/S0167-4838(00)00229-6;
RA	Takatsuka H., Sakurai Y., Yoshioka A., Kokubo T., Usami Y., Suzuki M.,
RA	Matsui T., Titani K., Yagi H., Matsumoto M., Fujimura Y.,
RT	"Molecular characterization of L-amino acid oxidase from Agkistrodon
RT	halsys blomhoffii with special reference to platelet aggregation.";



RT rhodostoma:comparative sequence analysis and characterization of  
RT active and inactive forms of the enzyme.";  
RL Eur. J. Biochem. 268:1679-1686(2001).  
RN [2]  
RP SEQUENCE OF 19-38 FROM N.A.  
RC TISSUE=Venom;  
RX MEDLINE=94361525; PubMed=8080286; DOI=10.1006/abbi.1994.1401;  
RA Ponudurai G., Chung M.C.M., Tan N.-H.;  
RT "Purification and properties of the L-amino acid oxidase from Malayan  
pit viper (Calloselasma rhodostoma) venom.";  
RL Arch. Biochem. Biophys. 313:373-378 (1994).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND CARBOHYDRATE-LINKAGE SITES.  
RC TISSUE=Venom;  
RX MEDLINE=20402326; PubMed=10944103; DOI=10.1093/emboj/19.16.4204;  
RA Pawelek P.D., Cheah J., Coulombe R., Macheroux P., Ghisla S.,  
RA Vrieland A.;  
RT "The structure of L-amino acid oxidase reveals the substrate  
trajectory into an enantiomerically conserved active site.";  
RL EMBO J. 19:4204-4215(2000).  
CC -|- FUNCTION: Catalyzes an oxidative deamination of predominantly  
hydrophobic and aromatic L-amino acids. Has an antibacterial  
effect and an ability to induce apoptosis. The H(2)O(2) produced  
by L-amino acid oxidation is involved in the apoxin-I induced  
apoptosis and hemorrhage caused by the venom.  
CC -|- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid  
+ NH(3) + H(2)O(2).  
CC -|- COFACTOR: FAD.  
CC -|- SUBUNIT: Homodimer.  
CC -|- MISCELLANEOUS: Has a pH optimum of 9.0, a determined pI of 4.4 and  
is temperature stable.  
CC -|- SIMILARITY: Belongs to the flavin monooxygenase oxidase family.  
CC Strong, to mammalian FICL.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AJ271725; CAB71136.1; ..  
DR PDB; 1F8R; X-ray; A/B/C/D=19-516.  
DR PDB; 1F8S; X-ray; A/B/C/D/E/F/G/H=19-516.  
DR GlycoSuiteDB; P81382; ..  
DR InterPro; IPR000759; Adrndx\_reductase.  
DR InterPro; IPR001613; Amineoxid.fl.  
DR InterPro; IPR002937; Amino\_oxidase.  
DR InterPro; IPR000205; NAD\_BS.  
DR Pfam; PF01593; Amino\_oxidase; 1.  
DR PRINTS; PR00419; ADXRDTASE.  
DR PRINTS; PR00757; AMINEOXDASEF.  
KW 3D-structure; Direct protein sequencing; FAD; Flavoprotein;  
KW Glycoprotein; Oxidoreductase; Signal; Toxin.  
FT SIGNAL 1 18  
FT CHAIN 19 516 L-amino-acid oxidase.  
FT NP\_BIND 52 108 FAD (ADP part) (Potential).  
FT CARBOHYD 190 190 N-linked (GlcNAc...).  
FT CARBOHYD 379 379 N-linked (GlcNAc...).  
FT CONFLICT 28 28 C -> E (in Ref. 2).  
FT CONFLICT 33 33 D -> N (in Ref. 2).  
FT TURN 24 25  
FT HELIX 26 29  
FT TURN 32 33  
FT HELIX 34 43  
FT STRAND 53 57  
FT STRAND 60 60  
FT HELIX 61 72  
FT TURN 73 74  
FT STRAND 76 80  
FT TURN 87 87  
FT TURN 88 89

FT STRAND 92 95  
FT TURN 96 99  
FT STRAND 100 103  
FT STRAND 109 110  
FT TURN 111 112  
FT HELIX 114 122  
FT TURN 123 124  
FT STRAND 127 130  
FT TURN 135 136  
FT STRAND 138 141  
FT TURN 142 143  
FT STRAND 144 147  
FT HELIX 148 153  
FT TURN 155 158  
FT HELIX 164 168  
FT TURN 171 178  
FT TURN 179 179  
FT HELIX 180 188  
FT HELIX 191 197  
FT TURN 198 199  
FT STRAND 202 202  
FT HELIX 203 209  
FT TURN 210 210  
FT HELIX 215 224  
FT TURN 225 226  
FT TURN 228 230  
FT HELIX 231 232  
FT TURN 234 234  
FT STRAND 235 245  
FT TURN 246 247  
FT STRAND 251 254  
FT TURN 255 256  
FT TURN 258 259  
FT HELIX 260 268  
FT TURN 269 269  
FT HELIX 270 272  
FT STRAND 273 274  
FT STRAND 278 284  
FT STRAND 289 294  
FT STRAND 302 305  
FT STRAND 307 310  
FT HELIX 314 317  
FT TURN 318 319  
FT STRAND 321 323  
FT HELIX 328 336  
FT STRAND 339 340  
FT STRAND 342 349  
FT HELIX 353 357  
FT TURN 358 358  
FT STRAND 363 366  
FT TURN 369 370  
FT STRAND 372 374  
FT TURN 381 382  
FT STRAND 385 392  
FT HELIX 393 397  
FT TURN 398 401  
FT HELIX 404 418  
FT TURN 419 420  
FT HELIX 423 429  
FT STRAND 430 437  
FT HELIX 438 440  
FT TURN 442 444  
FT STRAND 448 449  
FT TURN 453 454  
FT HELIX 455 464  
FT STRAND 467 467  
FT TURN 468 469  
FT STRAND 470 472  
FT HELIX 475 477  
FT HELIX 484 503  
SQ SEQUENCE 516 AA; 58221 MW; 5F943571083A3BDE CRC64;

Query Match

39.9%; Score 1079.5; DB 1; Length 516;

Best Local Similarity 44.4%; Pred. No. 2e-58;		Best Local Similarity 44.0%; Pred. No. 2e-57;	
Matches 219; Conservative 92; Mismatches 175; Indels 7; Gaps 5;		Matches 218; Conservative 96; Mismatches 169; Indels 13; Gaps 7;	
QY	33 LADCLDQDYDTLLQTLONGLPHINTSHHVIVGVAGMAGLTAAKLQDAGHTVTTILEAND 92	QY	33 LADCLDQDYDTLLQTLONGLPHINTSHHVIVGVAGMAGLTAAKLQDAGHTVTTILEAND 92
DB	25 LAECFDEYEEFETARNGLKATSPKPKVIVGVAGMAGLSAAVILAGAGHQVTVLEASE 84	DB	25 LEECFRETDYBEFLEIAKKNGLTATSNPKRVIVGVAGMAGLSAAVILAGAGHQVTVLEASE 84
QY	93 RVGGRVETYNKEGWAEMGAMRIPSSHRIQVQFVKKLGVENMFVMTDDNTFYLVNGV 152	QY	93 RVGGRVETYNKEGWAEMGAMRIPSSHRIQVQFVKKLGVENMFVMTDDNTFYLVNGV 152
DB	85 RFGGRVETYNKEGWAEMGAMRIPSSHRIQVQFVKKLGVENMFVMTDDNTFYLVNGV 144	DB	85 RVGGRVETYNKEGWAEMGAMRIPSSHRIQVQFVKKLGVENMFVMTDDNTFYLVNGV 142
QY	153 RERTYVQENPDVLYKNNVSESEKISADLLDRALOKVKEVEANGCKAALKYDRYSVK 212	QY	153 RERTYVQENPDVLYKNNVSESEKISADLLDRALOKVKEVEANGCKAALKYDRYSVK 212
DB	145 RKKVGEVKDPGLKYPVPSPBAGKSAGQLYEESLGKVEELKRTNCSYILNKYDTYSTK 204	DB	143 RKRREVKNPNGLLEYPVKPSEEGKSAQAQLYVESLRKVVVKELKRTNCKYILDKYDTYSTK 202
QY	213 EYLKEGGSLPGAVRMIGDGLLNEQSLMYTALSEMIYDQADVNDVSYTYHEVTGSDLLPEA 272	QY	213 EYLKEGGSLPGAVRMIGDGLLNEQSLMYTALSEMIYDQADVNDVSYTYHEVTGSDLLPEA 272
DB	205 EYLKEGGSLPGAVRMIGDGLLNEQSLMYTALSEMIYDQADVNDVSYTYHEVTGSDLLPEA 264	DB	203 EYLLKEGSLPGAVRMIGDGLLNEQSLMYTALSEMIYDQADVNDVSYTYHEVTGSDLLPEA 262
QY	273 FLSDVDPILLNSKVHQRQSDKGVIVSYQTGNESLMDSADIIVLVTTTAKAALFIDPD 332	QY	273 FLSDV--DVPILLNSKVHQRQSDKGVIVSYQT--GNESLMDSADIIVLVTTTAKAALFI 329
DB	265 MYRDIQDKVHFAVQVYIKIQNDQKVTYVYETLSKET--PSVTADYIVVCTTSRAVLIKFN 323	DB	263 MYEAIKEKVQVHFAVQVYIKIQNDQKVTYVYETLSKET--SVTADYIVVCTTSRAARI 320
QY	333 PPLSTSKMBALRSVHYDSSTKILLTRDKFWEDDGIKRGKSTIDGFSRVIYYPSPSHFN 392	QY	330 DFDPLSTSKMBALRSVHYDSSTKILLTRDKFWEDDGIKRGKSTIDGFSRVIYYPSPSHF 389
DB	324 PELLPPKAHALRSVHYDSSTKILLTRDKFWEDDGIKRGKSTIDGFSRVIYYPSPSHFN 382	DB	321 KPEPPLPPKAHALRSVHYDSSTKILLTRDKFWEDDGIKRGKSTIDGFSRVIYYPSPSHF 380
QY	393 ETIGVLLASYTWSDESLLFLGASDBELKELALDLAKIH--GEQWMDKCTGVIVVKWSA 449	QY	390 HTNETIGVLLASYTWSDESLLFLGASDBELKELALDLAKIH--GEQWMDKCTGVIVVK 446
DB	383 -GVGVIIA-YGIGDDANFFQALDFKDCADIVNDLSLHQLPKDIOQSCYPSVTKQWSL 440	DB	381 TSG--VGVIIA-YGIGDDANFFQALDFKDCADIVNDLSLHQLPKDIOQSCYPSVTKQWSL 437
QY	450 DPYSLGAFALFTPYQHLEVAQELFSEGRVHFAGEHTAPPHAWIETSMKSAIRAATNINK 509	QY	447 WSADPYSLGAFALFTPYQHLEVAQELFSEGRVHFAGEHTAPPHAWIETSMKSAIRAATN 506
DB	441 DKYAMGGITTTFTPYQHFSEALTAQGRYIYFAGEYTAQAHGWIDSTIKSGLRARDVNL 500	DB	438 WSLDYAMGGITTTFTPYQHFSEALTAQGRYIYFAGEYTAQAHGWIDSTIKSGLTARD 497
QY	510 VYANEESTIEHTKTD 522	QY	507 INKVANEESTIEHTKTD 522
DB	501 ASENPSGIHLSND 513	DB	498 VNRASENPSGIHLSND 513
RESULT 6		RESULT 7	
Q9PMC9	PRELIMINARY; PRT; 516 AA.	Q6TGO9	PRELIMINARY; PRT; 497 AA.
AC	Q9PMC9;	AC	Q6TGO9;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	FAD-containing L-amino acid oxidase Apoxin 1.	DE	L-amino acid oxidase (Fragment).
OS	Crotalus atrox (Western diamondback rattlesnake).	OS	Bothrops jararacussu (Jararacussu).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;	OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Viperidae; Crotalinae; Crotalus.	OC	Viperidae; Crotalinae; Bothrops.
OX	NCBI_TaxID=8730;	OX	NCBI_TaxID=8726;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	TISSUE=Venom gland;	RA	Soares A.M., Kashima S., Roberto P.G., Astolfi-Filho S., Pereira J.O.,
RA	Torii S., Mashima T., Naito M., Haga N., Yamane K., Yamamoto K.,	RA	Giglio J.R., Franca S.C.;
RA	Fox J.W., Tsuruo T.;	RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.	RL	EMBL; AY398691; AAR31182.1; -.
DR	EMBL; AF093248; AAD45200.1; -.	DR	GO; GO:0004497; F:monooxygenase activity; IEA.
DR	HSSP; P81382; 1F8R.	DR	GO; GO:0006118; P:electron transport; IEA.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.	DR	InterPro; IPR000759; Adrnx_reductase.
DR	InterPro; IPR000759; Adrnx_reductase.	DR	InterPro; IPR000960; Flav_cont_mnoxgn.
DR	InterPro; IPR002937; Amino_oxidase.	DR	InterPro; IPR0001613; Aminooxid_fl.
DR	InterPro; IPR000205; NAD_BS.	DR	PRINTS; PR00419; ADXRDTASE.
DR	InterPro; IPR00103; Pyridine_redox_2.	DR	PRINTS; PR00757; AMINEOXDASEF.
DR	Pfam; PF01593; Amino_oxidase; 1.	DR	PRINTS; PR00370; FMOXYGENASE.
DR	PRINTS; PR00419; ADXRDTASE.	FT	NON_TER 497 497
DR	PRINTS; PR00469; PNDRDTASEII.	SQ	SEQUENCE 497 AA; 56288 MW; 51AFCEB28038399A1 CRC64;
SQ	SEQUENCE 516 AA; 58766 MW; 6CB90A49A0C015E5 CRC64;		
Query Match 39.3%; Score 1063.5; DB 2; Length 516;		Query Match 39.2%; Score 1059.5; DB 2; Length 497;	
Best Local Similarity 45.1%; Pred. No. 3.3e-57;		Best Local Similarity 45.1%; Pred. No. 3.3e-57;	

Matches 212; Conservative 85; Mismatches 166; Indels 7; Gaps 4;

QY 33 LADCLEDDYDITLLQTLNDLPHINTSHHVIVGVAGMAGLTAAKLQDAGHTVILEAND 92  
DB 20 LEECFRETDYEEFLEIAKNGLTSTNPKEVIVGVAGMAGLSAAYVLNAGHQVTVLEASE 79

QY 93 RVGGRVETVRNKEGWAEMGAMRIPSSHRIVQVFKVLGVEMNEFVMTDDNTFYLVNGV 152  
DB 80 RAGGQVKTVRNKEGWAEMGAMRIPSSHRIVQVFKVLGVEMNEFVMTDDNTFYLVNGV 139

QY 153 RERTYVVOENPDVLYKNVSEKGI SADDLLDRAKQKVEEANGCKAALEKYDRYSVK 212  
DB 140 RRRGEVNDKPGVLDYVPKPVSEVGSAGLYEELQKAVEELRRNVCNMYLNLKDYTSTK 199

QY 213 EYLKEEGGLSPGAVRMIGDNLNEQSLMTYALSEMIYDOADVNDSTVYHEVTGSGDLLPEA 272  
DB 200 EYLLKEGNLSPGAVRMIGDNLNEQSLMTYALSEMIYDOADVNDSTVYHEVTGSGDLLPEA 259

QY 273 FLUSVLDVPIILNSKVKHQRQSKGVIVSYQTGNESSLMDLSADIVLVTTTAKAALFIDFD 332  
DB 260 MYAQIAQEKVHLNARVIKIQDQVKEVTYQT-SEKETLSVTADYIVVICTTSRAARRIKFE 318

QY 333 PPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGI RGGKSTIDGSPRYIYPSHSFHTN 392  
DB 319 PPLPKKAHALRSVHYDSSTKILLTFRDKFWEDDGI RGGKSTIDGSPRYIYPSHSFHTN 378

QY 393 ETIGVLLASYTWSDESLLFLGASDBELKELALDLAKIH--GEQWMDKCTGVIVKWSA 449  
DB 379 --VGVIIA-YGIGDDANFFQALDPKOCADIVINDLSLHLPKEDIOFTCHPMSIQR 435

QY 450 DYSISGAFALFTPYQHLEYAQELFSSEGRVHFACEHTAPPHAWIETSMKSAIRATN 499  
DB 436 DRYAMGGITTTPTYPQHFSEALTAPVDRIYPAGEVTAQAAGHWIASTIKS 485

RESULT 8

OXLA CROAD STANDARD; PRT; 516 AA.

AC O93364;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE L-amino-acid oxidase precursor (EC 1.4.3.2) (LAO) (LAO) (Apoxin I).  
OS Crotalus adamanteus (Eastern diamondback rattlesnake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Crotalus.  
OX NCBI\_TaxID=8729;

SEQUENCE FROM N.A., AND SEQUENCE OF 19-44 AND 106-130.

RP TISSUE=Venom;  
RC MEDLINE=98369573; PubMed=9703950; DOI=10.1006/bbrc.1998.9024;  
RX Raibekas A.A., Massey V.;  
RA "Primary structure of the snake venom L-amino acid oxidase shows high  
RT homology with the mouse B cell interleukin 4-induced Fgl protein.";  
RL Biochem. Biophys. Res. Commun. 248:476-478 (1998).  
CC -!- FUNCTION: Catalyzes an oxidative deamination of predominantly  
CC hydrophobic and aromatic L-amino acids. Has an antibacterial  
CC effect and an ability to induce apoptosis. The H(2)O(2) produced  
CC by L-amino acid oxidation is involved in the apoxin-I induced  
CC apoptosis and hemorrhage caused by the venom.  
CC -!- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid  
CC + NH(3) + H(2)O(2).  
CC -!- COFACTOR: FAD.  
CC -!- SUBUNIT: Homodimer.  
CC -!- PTM: Glycosylated.  
CC -!- SIMILARITY: Belongs to the flavin monooxygenase family.  
CC Strong, to mammalian FPGI.  
CC -!- DATABASE: NAME=Worthington enzyme manual;  
CC WWW="http://www.worthington-biochem.com/LAO/".  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.eib-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL; AF071564; AAC32267.1; -.  
DR PIR; J02066; JE0266.  
DR HSSP; P81382; 1F8R.  
DR InterPro; IPR000759; Admox\_reductase.  
DR InterPro; IPR002937; Amino\_oxidase.  
DR InterPro; IPR002050; NAD\_BS.  
DR InterPro; IPR00103; Pyridine\_redox\_2.  
DR Pfam; PF01593; Amino\_oxidase; 1.  
DR PRINTS; PR00419; ADXRDTASE.  
DR PRINTS; PR00469; PNDRDTRASEII.  
KW Antibiotic; Apoptosis; Direct protein sequencing; FAD; Flavoprotein;  
KW Glycoprotein; Oxidoreductase; Signal; Toxin.  
FT CHAIN 1 18 L-amino-acid oxidase.  
FT NP\_BIND 19 516 FAD (ADP part) (Potential).  
FT CARBOHYD 52 106 N-linked (GlcNAc...) (Potential).  
FT SEQUENCE 379 379 PDFAA77A49FDA05A\_CRC64;  
SQ SEQUENCE 516 AA; 58662 MW; PDFAA77A49FDA05A\_CRC64;

Query Match 39.2%; Score 1059.5; DB 1; Length 516;  
Best Local Similarity 44.0%; Pred. No. 3.5e-57;  
Matches 218; Conservative 94; Mismatches 171; Indels 13; Gaps 7;

QY 33 LADCLEDDYDITLLQTLNDLPHINTSHHVIVGVAGMAGLTAAKLQDAGHTVILEAND 92  
DB 25 LEECFRETDYEEFLEIAKNGLTATSNPKRVIVGVAGMAGLSAAYVLNAGHQVTVLEASE 84

QY 93 RVGGRVETVRNKEGWAEMGAMRIPSSHRIVQVFKVLGVEMNEFVMTDDNTFYLVNGV 152  
DB 85 RVGGRVETVRNKEGWAEMGAMRIPSSHRIVQVFKVLGVEMNEFVMTDDNTFYLVNGV 142

QY 153 RERTYVVOENPDVLYKNVSEKGI SADDLLDRAKQKVEEANGCKAALEKYDRYSVK 212  
DB 143 RKRVRVKNPGLLEYVPKPVSEKSAQLYVESLRKVBEELRSTNCKYILDKYDTYSTK 202

QY 213 EYLKEEGGLSPGAVRMIGDNLNEQSLMTYALSEMIYDOADVNDSTVYHEVTGSGDLLPEA 272  
DB 203 EYLLKEGNLSPGAVRMIGDNLNEQSLMTYALSEMIYDOADVNDSTVYHEVTGSGDLLPEA 262

QY 273 FLUSVLDVPIILNSKVKHQRQSKGVIVSYQT-NESSLMDLSADIVLVTTTAKAALFI 329  
DB 263 MYEAIKEKVQHFNARVIEIQNDREATVYQTSANEMS--SVTADYIVVICTTSRAARRI 320

QY 330 DFDPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGI RGGKSTIDGSPRYIYPSHSF 389  
DB 321 KFEPPLPKKAHALRSVHYDSSTKILLTFRDKFWEDDGI RGGKSTIDGSPRYIYPSHSF 380

QY 390 HTNETIGVLLASYTWSDESLLFLGASDBELKELALDLAKIH--GEQWMDKCTGVIVK 446  
DB 381 TSG--VGVIIA-YGIGDDANFFQALDPKOCADIVINDLSLHLPKEDIOFTCHPMSIQR 437

QY 447 WSADPYSLGAFALFTPYQHLEYAQELFSSEGRVHFACEHTAPPHAWIETSMKSAIRATN 506  
DB 438 WSLDKYAMGGITTTPTYPQHFSEALTAPPKRIYFACEYTAQFHGWDSTIKSLGLTAARD 497

QY 507 INKVAANEESTIEHTKD 522  
DB 498 VNRASENPSGIHLNSD 513

RESULT 9

Q6TQ08  
ID Q6TQ08 PRELIMINARY; PRT; 478 AA.  
AC Q6TQ08;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE L-amino acid oxidase (fragment).





05-JUL-2004 (Rel. 44, Last annotation update)  
 Interleukin-4 induced protein 1 precursor (Fig-1 protein) (mFig1).  
 Name=11411; Synonyms=Fig1;  
 Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C, and CBA/J;  
 RX MEDLINE=97225983; PubMed=9122225; DOI=10.1073/pnas.94.6.2507;  
 RA Chu C.C., Paul W.E.;  
 RT "Fig1, an interleukin 4-induced mouse B cell gene isolated by cDNA  
 RT representational difference analysis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:2507-2512(1997).  
 RN [2]  
 RN SEQUENCE OF 122-289 FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Spleen;  
 RX MEDLINE=99012997; PubMed=9798653; DOI=10.1016/S0161-5890(98)00031-5;  
 RA Chu C.C., Paul W.E.;  
 RT "Expressed genes in interleukin-4 treated B cells identified by cDNA  
 RT representational difference analysis.";  
 RL Mol. Immunol. 35:487-502(1998).  
 RN [3]  
 RN SEQUENCE OF 217-630 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryonic head;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gusicinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J.J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Welle C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yaeunichi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 CC -I- COPACTOR: FAD (Potential).  
 CC -I- INDUCTION: By interleukin-4.  
 CC -I- SIMILARITY: Belongs to the flavin monooxygenase family.  
 CC Strong, to snake L-amino acid oxidase.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 CC EMBL; U70429; AAB51353.1; -;  
 DR EMBL; U70430; AAB51354.1; -;  
 DR EMBL; U89428; AAC36534.1; -;  
 DR EMBL; U89429; AAC36535.1; -;

DR EMBL; AK014297; BAB29253.1; ALT\_INIT.  
 DR HSSP; P81382; 1F8R.  
 DR MGD; MG1:109552; IL4i1.  
 DR InterPro; IPR000759; Adrxndx\_reductase.  
 DR InterPro; IPR001613; Amino\_oxidase.  
 DR InterPro; IPR002937; Amino\_oxidase.  
 DR InterPro; IPR000205; NAD\_BS.  
 DR Pfam; PF01593; Amino\_oxidase; 1.  
 DR PRINTS; PR00419; ADXRDTASE.  
 DR PRINTS; PR00757; AMINOXADASEF.  
 KW FAD, Flavoprotein; Oxidoreductase; Signal.  
 FT SIGNAL 1 21 Potential.  
 FT CHAIN 22 630 Interleukin-4 induced protein 1.  
 FT NP\_BIND 59 115 FAD (ADP part) (Potential).  
 FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 219 219 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 385 385 R -> Q (in Ref. 3).  
 FT CONFLICT 598 630 PSEHVQVHGEVPEWHGHGSGTTPQVHRVDHS -> LRSM  
 YRCMGKSSLSGVMGDLAPRKCTGTTNPKKEEVSTQLLS  
 QPSSGQTDHLH (in Ref. 3).  
 FT SQ SEQUENCE 630 AA; 70190 MW; A674C5D60D89A071 CRC64;  
 Query Match 38.3%; Score 1034; DB 1; Length 630;  
 Best Local Similarity 43.5%; Pred. No. 1.7e-55;  
 Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;  
 QY 26 ALSLSKHLADCLDXYDTLLQTLQDGLPHINTSHHVIVGVAGMAGLTAAKLLDAGHTV 85  
 DB 25 AASSLNPLEKCMEDHEDYDQLLVVTGLNRTSKPKQVYVGVAGVAGLVAAKMLSDAGHKV 84  
 QY 86 TLELANDRVGRVETRYNEKEGWAEAMGMRIPSSSHRVVQVFKVLGVEMNPFVMTDDNT 145  
 DB 85 TLELANDRIGRIFTRFEKGTWIGELGAMWPSHRLHLKLCRTLGLNLTQFYDENT 144  
 QY 146 FYLVNGVRETYVVOENPDVLKYNVSEKGISADLLDRLAQVKVEEVEANGCKAALEK 205  
 DB 145 WTEVHNKLVNRYVVEKMEKLGYNLNNRERGHSPEDIVQMALNKAFKDLKALGCKKAMNK 204  
 QY 206 YDRSVKYLEKEEGLSGVARMIGDNLNEQSLMYTALSEMIYDQDVNDVSYTVEHTGG 265  
 DB 205 FNKHTLLEEEGNLSRPVOLLGDVMSBEGFFYLSFAELRAHACLSDRURYSRIVGG 264  
 QY 266 SDLLPEAFSLVDVPIILNLSKVHQRQDKGVIVSYQTGNSSLLMDLSADIVLVTTTAKA 325  
 DB 265 WDLPLRALLSSLSGALLNAPVSVITQGRNDRVHIATSLHSE-KTLTADVLLTASGPA 323  
 QY 326 ALFIDFDPLSISKWEALRSVHYDSSTKILLTFRDKFWEDDGIRGKSIITDGPRIYYYP 385  
 DB 324 LQRTFSPPLTRKQREALRHLHYVAASKVFLSFRFPFWHEEHIEGHSNTDRPSRLIYP 383  
 QY 386 SHSFHTNETIGVLLASYTMSDESLLFLCASDEELKELALDRLAKIHGE---QVWDKCTGV 442  
 DB 384 ARGEGS-----LLLSASYTMSDAAAAPFAGLSLTDQTLRLVLQDVAAHLPPVFLWDG-RGV 437  
 QY 443 IVKWSADPYSIGALFALFPTQHLLEYAQELSSSE-GRVHFAGEHTAFPHAWTETSMKSAI 501  
 DB 438 -VKRAEDPHSQGGFVQPPPLYGREAEDYDSAPGRIYFAGEHTALPHGWVETAVKSL 496  
 QY 502 RAATNIN 508  
 DB 497 RAAVRIN 503  
 RESULT 14  
 Q6YBV6  
 ID Q6YBV6 PRELIMINARY; PRT; 630 AA.  
 AC Q6YBV6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Interleukin-4 induced gene-1 protein.  
 GN Name=11411;

OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MRL;
RA	Chu C.C., Kim J.A., Hsueh K.;
RL	Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY161348; AAC23118.1; -
DR	GO; GO:0016491; F:oxygen reductase activity; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
DR	InterPro; IPR000759; Adrnx_reductase.
DR	InterPro; IPR001613; Amino oxid fl.
DR	InterPro; IPR002937; Amino oxidase.
DR	Pfam; PF01593; Amino oxidase; 1.
DR	PRINTS; PR00419; ADXEDTASE.
DR	PRINTS; PR00757; AMINEOXDASEF.
SQ	SEQUENCE 630 AA; 70162 MW; 667515D608D93955 CRC64;

  

Query Match	38.3%;	Score 1034;	DB 2;	Length 630;
Best Local Similarity	43.5%;	Pred. No. 1.7e-55;		
Matches	212;	Conservative 100;	Mismatches 163;	Indels 12; Gaps 6;

  

Qy	26	ALSLSKEHLADCLEKDYDTLLQTLDNLGPHNTSHHVIVVGAGMAGLTAAKLLODAGHTV	85
Dd	25	AASLNPIEKMEDHYEQLLKVVTLGLNRTSKPKQVVGVGAVGLVAARKWLSDAHGKV	84
Qy	86	TILSANDRVGGRVETYNKEKGWAENGAMRIPSHRIQVFVKVLGVMEHFVMTDNT	145
Dd	85	TILEADNRIGRIFTFRDEKTGWIGELGAMRPPSSRHILKLCRTLGLNLFTQTYDENT	144
Qy	146	FYLVNGVRERTYVVOENPDVLKYNVSEKGISADDLLDRALQKVGEVEANGCKAALEK	205
Dd	145	WTEVHNKLRNVVYEKPEKLGYNLNNRRCHSPEDIQMALNKAFDLKALGCKKAMNK	204
Qy	206	YDRYSVKEYLKBEGGLSPGAVRMITDLLNEQSMLYTALSEMIPDOADVNSVTYHEVTGG	265
Dd	205	FNKHITLEYLLEEGLNLRPAVOLLLGDVMSESGFFYLPFAEARAHACISDLRLYSRIYVG	264
Qy	266	SDLLPEAPFLSLVDVPILLNSVKVHKIRQSDKGVIVSYOTGNESLMDLSADTILVTTAKA	325
Dd	265	WDLLPRLALLSLGALLNAPVSVITQRNDVRVHIATSLHSE-KTUTADVLLLTASGPA	323
Qy	326	ALFIDFPDPPLSIKWEALRSVHYDSSTKILLTFRDKFEDDGIRGKSITDGPSTRYYYP	385
Dd	324	LQRTTFPPLTRKRQEALRALHALHYVAASKVLFSPFRPFWEHHIEGHGHSNDRPSSLFYF	383
Qy	386	SHSFHTNETTGVLASTWSDESLLFLGASDEELKELALDLAKIHGE---QWWDKTCGV	442
Dd	384	AQSEGSG-----LLLASVYTWSDAAAPPAGLSDDQTLRLVLQDVAAALHGFVFLRWDMG-RGV	437
Qy	443	IWKWSADPYSLGAFALFTPYOHEYAEQLFSSE-GRVHPAGEHTAFPRAWIETSMKSAI	501
Dd	438	-VKWEADPHSQGGFVQPPLYGREADEYDWSAPFGRIYFAGEHTALPHGWVETAVKSGL	496
Qy	502	RAATNIIN 508	
Dd	497	RAAVRIN 503	

RESULT 15	
Q6YDI8	
ID	Q6YDI8
	PRELIMINARY;
ID	Q6YDI8
	AC
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Interleukin-4 induced gene-1 protein.
GN	Name=Il4l1;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NZW;
RA	Chu C.C., Kim J.A., Hueh K.;
RL	Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY157538; AA017039.1; -.
DR	EMBL; AY157537; AA017038.1; -.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
DR	InterPro; IPR000759; Adrnxn reductase.
DR	InterPro; IPR001613; Aminooxid fl.
DR	InterPro; IPR002937; Amino oxidase.
DR	InterPro; IPR000205; NAD_BS.
DR	Fram; PFO1593; Amino oxidase; 1.
DR	PRINTS; PR00419; ADXRDTASE.
DR	PRINTS; PR00757; AMINEOXDASEF.
SQ	SEQUENCE 630 AA; 70294 MW; 5A90C0CB1B29D9095 CRC64;

Query Match	38.3%;	Score 1034;	DB 2;	Length 630;
Best Local Similarity	43.5%;	Pred. No. 1.7e-55;		
Matches	212;	Conservative 100;	Mismatches 163;	Indels 12; Gaps 6;
Qy	26	ALSLSKEHLADCLDEKDYDTLLQTLNDGLPINTSHHVIVYAGWAGITAAKLLDAGHTV	85	
Db	25	AASLNPDEIKCMBDHYEQLLKVVTLGLNRTSKPKQVYVVGAGVAGILVAAKMLSDAGHKV	84	
Qy	86	TILEANDRVGGRVETRYRNEKEGWAEVGMAMRIIPSSHRIVQVFWVKLGVMENFVMTDNT	145	
Db	85	TILEADNRIGGRIFTFREDEKTGIVGELGANRMPSSHRIHLKRLTGLNLTOFTQYDENT	144	
Qy	146	FYLVNGVRETYVYQSNPDVLKYNVSESEKGISADLLDRALOKVKEEVEANGCAALEK	205	
Db	145	WTEVHNVKLRNVYVVKMPEKLGYNLNRREHSPEDIYQNALNKAFKDLKALGCKKAMNK	204	
Qy	206	YDRYSVKEYIKERGGISPGAVRMIGDLLNEQSLMYTALSEMIYDQADVDSNVYHEVTGG	265	
Db	205	FNKHTLLEYLLEEGNISRPVQLGLDGVMSSEGFYLSFAEALRAHACLSDRLRYSRIVGG	264	
Qy	266	SDLLPEAFSLVDVPIILNLSKVKHIRQSKGVTVSVQTGNESLMDLSADIVLVTTTAKA	325	
Db	265	WDLPLRALSSLGALLNAPVSVITQGRNDVRVHATLSLSE-KTLTADVLLTAGSPA	323	
Qy	326	ALFIDFDPPLSUSKMBALRSVHVYDSTKILLTPRDKFWDGDRGKGSITDGSPRYIYYP	385	
Db	324	LQRITFSPPLTRQRBQALRALHYVAASKVFLSPRPFWHEEHTEGGHSNDRPSRLTFYP	383	
Qy	386	SHSFHNETIGVLLASVYTSWDSDESLFLGASDEELKELARLDLAKIHGE---QWMDKCTGV	442	
Db	384	ARGEGS-----LULASYTWSDAAPFAGLSTDTQLRLVLQDVAAALGPPVFRLWDG-RGV	437	
Qy	443	IVKWSADPYSYLGAFALFTPYQHLEYAQVLFSSSE-GRVHFAGBHTAPPFAHWIETSMKSAI	501	
Db	438	-VKRWAEDPHSQGGFVVQPLYGCREAEDYDWSAPFGRIYFAGEHTALPHGWVETAVKSGL	496	
Qy	502	RAATNIN	508	
Db	497	RAAVRIN	503	

Search completed: October 4, 2005, 14:00:54  
Job time : 193 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 13:43:40 ; Search time 79 Seconds  
(without alignments)  
1162.663 Million cell updates/sec

Title: US-10-645-094-1

Perfect score: 2703

Sequence: 1 MNLHVVKWKLVSUVSLITLY.....TNINKVANEESTIEHTKDEL 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 800245 seqs, 175286997 residues

Total number of hits satisfying chosen parameters: 800245

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New.\*

- 1: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	999	37.0	567	1	PCT-US03-28361-44
2	999	37.0	567	6	US-10-990-328A-11737
3	999	37.0	567	6	US-10-152-381B-476
4	999	37.0	567	7	US-11-025-607-84
5	407	15.1	478	6	US-10-166-087B-48
6	294	10.9	545	6	US-10-940-774A-11442
7	288	10.7	520	1	PCT-US05-09248-13
8	288	10.7	520	1	PCT-US03-10870-447
9	288	10.7	520	1	PCT-US03-10870-448
10	288	10.7	520	6	US-10-990-328A-8287
11	288	10.7	520	6	US-10-990-328A-8288
12	288	10.7	520	7	US-11-051-454-252
13	283	10.5	527	1	PCT-US05-09248-11
14	283	10.5	527	1	PCT-US03-10870-549
15	283	10.5	527	6	US-10-990-328A-8290
16	283	10.5	527	6	US-10-990-328A-8291
17	283	10.5	527	6	US-10-990-328A-8292
18	283	10.5	527	7	US-11-051-454-250
19	283	10.5	531	6	US-10-940-774A-11443
20	271	10.0	520	1	PCT-US05-11532-1348
21	271	10.0	890	7	US-11-097-143-25362
22	271	10.0	890	7	US-11-097-143-32703
23	263.5	9.7	730	1	PCT-US05-18850-1179
24	252.5	9.3	619	7	US-11-072-512-2472
25	238	8.8	906	6	US-10-450-763-51651

26	229	8.5	527	1	PCT-US03-10870-2456	Sequence 2456, Ap
27	221	8.2	513	6	US-10-218-141-1224	Sequence 1224, Ap
28	221	8.2	518	6	US-10-218-141-3192	Sequence 3192, Ap
29	220.5	8.2	583	7	US-11-097-143-17742	Sequence 17742, A
30	218.5	8.1	448	1	PCT-IB03-06509-4659	Sequence 4659, Ap
31	218.5	8.1	448	6	US-10-934-893-4659	Sequence 4659, Ap
32	205	7.6	558	6	US-10-501-098-1	Sequence 1, Appl
33	196.5	7.3	509	7	US-11-097-143-17202	Sequence 17202, A
34	187	6.9	502	7	US-11-097-143-42648	Sequence 42648, A
35	183.5	6.8	500	6	US-10-471-571A-3712	Sequence 3712, Ap
36	181.5	6.7	503	6	US-10-914-020-7202	Sequence 7202, Ap
37	175.5	6.5	421	6	US-10-501-098-2	Sequence 2, Appl
38	173	6.4	511	6	US-10-504-601-6	Sequence 6, Appl
39	173	6.4	511	6	US-10-152-381B-122	Sequence 122, App
40	170.5	6.3	504	6	US-10-504-601-4	Sequence 4, Appl
41	169.5	6.3	479	7	US-11-097-143-12792	Sequence 12792, A
42	169	6.3	502	6	US-10-471-571A-3706	Sequence 3706, Ap
43	166	6.1	476	7	US-11-097-143-11910	Sequence 11910, A
44	165.5	6.1	484	6	US-10-914-020-7130	Sequence 7130, Ap
45	165.5	6.1	512	7	US-11-100-328-19	Sequence 19, Appl

#### ALIGNMENTS

##### RESULT 1

PCT-US03-28361-44  
; Sequence 44, Application PC/TUS0328361  
; GENERAL INFORMATION:

; APPLICANT: GENENTECH, INC.  
; APPLICANT: SARAH C. BODARY  
; APPLICANT: HILARY CLARK  
; APPLICANT: BRISDELL HUNTE  
; APPLICANT: JANET K. JACKMAN  
; APPLICANT: JILL SCHOENFELD  
; APPLICANT: P. MICKY WILLIAMS  
; APPLICANT: WILLIAM I. WOOD  
; APPLICANT: THOMAS D. WU

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE  
; FILE REFERENCE: P1975R1-PCT

; CURRENT APPLICATION NUMBER: PCT/US03/28361  
; CURRENT FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: US 60/410,174  
; PRIOR FILING DATE: 2002-09-11

; NUMBER OF SEQ ID NOS: 104

; SEQ ID NO 44

; LENGTH: 567

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US03-28361-44

Query Match 37.0%; Score 999; DB 1; Length 567;  
Best Local Similarity 41.8%; Pred. No. 1.4e-65;  
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy	3	LHVVKWKLVSUVSLITLYSHT-VALSKLEHADCLDQDYDTLLQTLNDGLPHINTSHH	61
Db	6	LHL-----LVLVPIILLVSQDWKAERSQDPFKMOPDYEQLLKVVVTWGLNRTLKPOR	61
Qy	62	VVIYVAGMAGLTAAKLQDAGHTVTILEANDRVGGRVETRYRNEKEGWYAEMGMRIPSSH	121
Db	62	VIVVAGVAGLVAALKVLSADGKHVTILEADNRIGRIFTYRDQNTGIGELGAMRMPSSH	121
Qy	122	RIVQWFKVLGVENEFVMTDDNTFYLVNGVRERTYVQVNPDLVLYNVSSEKISADD	181
Db	122	RILHLKQGLGLNLTFTQYDKNTWTVEHVKLYNYYVVEKYPKELGYALRPOEKHSPED	181
Qy	182	LLDRALQKVKEEVANGCKALEKYDYRYSVKEYLKEGSLSPGAVRMTIGDLLNEOSLMT	241
Db	182	IYQMALNOALKALCGRCAMKPKFERHTLLEYLLGEGNLSRPVQLLLGDVMSDEGDFYL	241
Qy	242	ALSEMIYDQADVNDVSVTYHEVTGGSDLLPEAFLSVLDPILLNSKVKHQRSKGVIVSY	301



Qy	361	KF	WEDD	GIR	GK	S	ITD	G	S	R	V	I	Y	P	S	H	S	H	E	T	N	E	T	G	V	L	L	A	S	T	W	E	S	L	L	F	G	A	S	D	E	L	K	420											
Db	362	P	F	W	E	E	H	I	E	G	H	S	N	D	R	S	M	I	F	Y	P	-----	P	P	R	E	G	A	L	L	A	S	T	W	S	D	A	A	A	F	A	G	L	S	R	E	A	L	416						
Qy	421	E	L	A	L	R	D	L	A	K	I	N	G	-----	E	Q	W	M	D	K	T	G	V	I	V	K	W	S	A	D	P	Y	S	L	G	A	F	A	L	T	P	V	Q	H	E	V	A	Q	E	L	P	S	S	-	476
Db	417	R	L	A	L	D	V	A	A	L	H	G	P	V	P	Q	L	M	D	G	-	T	G	V	-	V	K	R	E	A	D	H	S	Q	G	F	V	Q	P	P	-----	A	L	M	O	T	E	K	466						
Qy	477	-----	G	R	V	H	A	G	H	T	A	P	P	H	A	I	E	T	S	M	K	S	A	I	R	A	A	T	N	-----	508																								
Db	467	D	M	T	V	P	G	R	I	V	E	A	G	H	T	A	P	P	H	G	V	E	T	A	V	K	S	A	L	R	A	A	I	K	-----	505																			

RESULT 4  
US-11-025-607-84  
; Sequence 84, Application US/11025607  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same

```

; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/11/025,607
; CURRENT FILING DATE: 2004-12-28
; PRIOR APPLICATION NUMBER: US/09/946,374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; REMAINING prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 84
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-025-607-84

```

[illegible]

```

RESULT 5
US-10-166-087B-48
; Sequence 48, Application US/10166087B
; GENERAL INFORMATION:
; APPLICANT: Ecopia Biosciences Inc.
; APPLICANT: Farnet, Chris
; APPLICANT: Staffa, Alfredo
; APPLICANT: Zazopoulos, Emmanuel
; TITLE OF INVENTION: NUCLEIC ACID
; TITLE OF INVENTION: ANTHRACYCIN
; FILE REFERENCE: 3014-2US
; CURRENT APPLICATION NUMBER: US/10/166,087B
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Streptomyces refuineus subspecies thermotolerans
US-10-166-087B-48

```

Query Match	15.1%	Score 407;	DB 6;	Length 478;
Best Local Similarity	29.2%;	Pred. No. 7.5e-22;		
Matches 144;	Conservative 83;	Mismatches 196;	Indels 70;	Gaps 20;
Qy	47	QTLNGLPHINTSHHVVIVGAGMAGTAAKLLQDAGHTVLTLEANDVGGRVETRYNE-K 105		
Db	11	ETFDSGIPQHGTSVVIVGAGLAGLAAAHLETFQGVTVTVLEADSPGGRTWTLREPPA 70		
Qy	106	EGHYAEMGAMRIPSSHRIVQVFVKKLGVENNEFMTDDNTFYLVNGVRERYTVVQENPDV 165		
Db	71	DGLRAAGAMTVTEHCHYTMHYLKENGIGTEPSDLVDTDFGYRNRGVRIPDPKVGGEHADL 130		

```

166 LKYNVSESEKGISADLLDRALOKKVEAVEANGKAA-----LEKYDRYSKEYLK 216
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
131 L--GLHPDERHLTVEGMIARYVTFENEKL--GPEIAQVPWAPTRELLEDRVVRVLE 185
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
217 EEGG-----LSPCAVRMIGDLINEQSLMYTALSEMIDQADVDSVT--YHEVTGGS 266
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
186 ERGASAAAGLMEPPFLEMGRGELESASAMAWAR---YESGPRSFSTAGAOWYKEGGT 241
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
267 DLLPEAFSLVDVPTILLNSKVKHIRQSDKGVTVSYOTGNESSIMDLSDIVLVTITAKAA 326
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 DMLABALASRLGERILYRKPVVRIAQDDREAQVTF--DHGRRLTLCADRVVVTAFSSM 299
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
327 LFIDPD-PPLSISKMEALRSVHYDSTKILLTRDKFW-----EDDIGRGKSIT-- 375
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
300 RRVNLSMARLSAAKHAARLRLRYASTVRVFLQMRKFWPERRLMLSTDVAVTVDATPH 359
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
376 -DGPSRYIYPSHSPHTNETIGVILASTWSDESLLFLCASDEELKELALROLAKI--HG 432
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
360 LPGPRRIV-----ECWLTG-----WQAAAAAM--SPEERVAVALNELEPILPGA 402
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
433 EQVWDKCTGVIVKWSADPYSLGAFALTPPYO-HLEYAQELFSSBGRVHFAGEHTAF-PH 490
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
403 RENFELGTSV---AWDNFYPAGAYIL--PEKXHSLEMAAIPAPGRHFAGEHTAFEPN 457
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
491 AW-IETSMKSAIR 502
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
458 GGSNNYALESSIR 470
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 6
US-10-940-774A-11442
; Sequence 11442, Application US/10940774A
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/10/940,774A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11442
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Human
US-10-940-774A-11442

```

[illegible]

✓

Db 315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHKARKLARL-----TKERLUKKUCELY 368  
Qy 423 -----ALRDLAKIHGEQWMDKCTGTVIVKKWSADPYSLGAFALFTPYQHL-EYAQELFSSE 476  
Db 369 AKVLGSLEALEPVHYEE-----KNWCEEQSGGCYTYFPFGILTYQGRVLRQPV 418  
Qy 477 GRVHFAGHTAPPH--AWIETSMKSAIRAATNI-----NKVANE 514  
Db 419 DRIYFAGTETA-THWSGYMEGAVEAGERAAREILHAMGKIPED 461

## RESULT 8

PCT-US03-10870-447  
; Sequence 447, Application PC/TUS0310870  
; GENERAL INFORMATION:  
; APPLICANT: Mitokor, Inc.  
; APPLICANT: Buck Institute  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: 660088.465PC  
; CURRENT APPLICATION NUMBER: PCT/US03/10870  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3025  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 447  
; LENGTH: 520  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-10870-447

Query Match 10.7%; Score 288; DB 1; Length 520;  
Best Local Similarity 25.0%; Pred. No. 5.4e-13;  
Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;  
Qy 62 VVIVGAGMAGLTAALKLQDAGHTVILEANDRVGRVETRYNEKEGYAEMGAMRI-PSS 120  
Db 7 VVVGGGSGMAAAKLLHDSGLNVVLEARDRVGGRTYTLRNQKVK-YVDLGGSYVGP 65  
Qy 121 HRIVQWFKVLGVE---MNEFVMTDDNTFYLVNGVRYRTYVVOE-----NPDVLKYNVS 171  
Db 66 NRILR-LAKELGLETYKNEVER-----LIHHVKGKSPRGPFPVWNP--ITY--- 112  
Qy 172 ESEKISADDDLLD-----RALQKVEEVEANG-CKAAL-EKYDRYSVKEYLKEEGLSPG 224  
Db 113 -----LDHNNFWRTDMDGREIPSDAPWKAFLAEEDWNTMKELL----- 152  
Qy 225 AVRMIGDLLNEOSLMYTALSEMIYDQADVNSVT--YHEVT----- 263  
Db 153 -----DKLCWTSKQL-ATLFVNLVCVTAETHEVSALWFLWYVKQCGGTTTIIIS 200  
Qy 264 -----GGSDLLPEAFSLVDVPILLNSKVKHRSQDKGVIVSYQTGNESSLMDL 312  
Db 201 TTNGQERKFGVGGSGVSEIRIMDLGDRVKLRPVIYIDQTRNVLV--ETLNHEM---Y 255  
Qy 313 SADVILVTTTAKAALFIDPPLPSISKMEALRSVHYDSSTKILLTFROKFWEDDGI 372  
Db 256 EAKYVISAIPPTLGKMHFNPLPMRNQMITRVLPSGVKICVIVYKFPFWKKDY-CGT 314  
Qy 373 SITDGPSRYIY-----PSHSFHTNETIGVLLASYTWSDESLLFLGASDEELKEL---- 422  
Db 315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHKARKLARL-----TKERLUKKUCELY 368  
Qy 423 -----ALRDLAKIHGEQWMDKCTGTVIVKKWSADPYSLGAFALFTPYQHL-EYAQELFSSE 476  
Db 369 AKVLGSLEALEPVHYEE-----KNWCEEQSGGCYTYFPFGILTYQGRVLRQPV 418

RESULT 10

Qy 477 GRVHFAGHTAPPH--AWIETSMKSAIRAATNI-----NKVANE 514  
Db 419 DRIYFAGTETA-THWSGYMEGAVEAGERAAREILHAMGKIPED 461

## RESULT 9

PCT-US03-10870-448  
; Sequence 448, Application PC/TUS0310870  
; GENERAL INFORMATION:  
; APPLICANT: Mitokor, Inc.  
; APPLICANT: Buck Institute  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: 660088.465PC  
; CURRENT APPLICATION NUMBER: PCT/US03/10870  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3025  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 448  
; LENGTH: 520  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-10870-448

Query Match 10.7%; Score 288; DB 1; Length 520;  
Best Local Similarity 25.0%; Pred. No. 5.4e-13;  
Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;  
Qy 62 VVIVGAGMAGLTAALKLQDAGHTVILEANDRVGRVETRYNEKEGYAEMGAMRI-PSS 120  
Db 7 VVVGGGSGMAAAKLLHDSGLNVVLEARDRVGGRTYTLRNQKVK-YVDLGGSYVGP 65  
Qy 121 HRIVQWFKVLGVE---MNEFVMTDDNTFYLVNGVRYRTYVVOE-----NPDVLKYNVS 171  
Db 66 NRILR-LAKELGLETYKNEVER-----LIHHVKGKSPRGPFPVWNP--ITY--- 112  
Qy 172 ESEKISADDDLLD-----RALQKVEEVEANG-CKAAL-EKYDRYSVKEYLKEEGLSPG 224  
Db 113 -----LDHNNFWRTDMDGREIPSDAPWKAFLAEEDWNTMKELL----- 152  
Qy 225 AVRMIGDLLNEOSLMYTALSEMIYDQADVNSVT--YHEVT----- 263  
Db 153 -----DKLCWTSKQL-ATLFVNLVCVTAETHEVSALWFLWYVKQCGGTTTIIIS 200  
Qy 264 -----GGSDLLPEAFSLVDVPILLNSKVKHRSQDKGVIVSYQTGNESSLMDL 312  
Db 201 TTNGQERKFGVGGSGVSEIRIMDLGDRVKLRPVIYIDQTRNVLV--ETLNHEM---Y 255  
Qy 313 SADVILVTTTAKAALFIDPPLPSISKMEALRSVHYDSSTKILLTFROKFWEDDGI 372  
Db 256 EAKYVISAIPPTLGKMHFNPLPMRNQMITRVLPSGVKICVIVYKFPFWKKDY-CGT 314  
Qy 373 SITDGPSRYIY-----PSHSFHTNETIGVLLASYTWSDESLLFLGASDEELKEL---- 422  
Db 315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHKARKLARL-----TKERLUKKUCELY 368  
Qy 423 -----ALRDLAKIHGEQWMDKCTGTVIVKKWSADPYSLGAFALFTPYQHL-EYAQELFSSE 476  
Db 369 AKVLGSLEALEPVHYEE-----KNWCEEQSGGCYTYFPFGILTYQGRVLRQPV 418  
Qy 477 GRVHFAGHTAPPH--AWIETSMKSAIRAATNI-----NKVANE 514  
Db 419 DRIYFAGTETA-THWSGYMEGAVEAGERAAREILHAMGKIPED 461

RESULT 10

```
US-10-990-328A-8287
; Sequence 8287, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8287
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-990-328A-8287

Query Match      10.7%; Score 288; DB 6; Length 520;
Best Local Similarity 25.0%; Pred. No. 5.4e-13;
Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;

QY 62 VVIVAGMAGLTAAKLLDAGHTVTLLEANDRVGGRVETYNKEGWAEGMAMRI-PSS 120
Db 7 VVVVGGSIGMAAKLLHDSGLNVVLEARDRVGGRTYTLRNQKVK-YVDLGGSYVGPTQ 65
QY 121 HRIVQMFVKKLGV---MNEFVMTDDNTFYLVNGVRERTYVQE-----NPDVLKYNVS 171
Db 66 NRILR-LAKELGLETYKNEVER-----LIHHVKGKSYPRGPPVWNP--ITY--- 112
QY 172 ESEKISADLLD-----RALQKVEEVEANG-CKAAL-EKYDRYSVKEYLKEEGLSPG 224
Db 113 -----LDHNNFWRTWDDMGREIPSDAPWKAPLAEWDNMTMKELL----- 152
QY 225 AVRMTGDLNQSMLYALTSEMIYDQADVDSVT--YHEVT----- 263
Db 153 -----DKLCWTESAKOL-ATLFVNLCVTAETHEVSALWFLVYVKQCGGTTIRIS 200
QY 264 -----GSDLLPEAFSLVDVPIILLNSKVKHQRSDKGVIVSYQTGNESLMDL 312
Db 201 TTNGQERKFGVGGQGVSEIRIMDLGDRVKLERPVYIDQRENVLV--ETLNHEM---Y 255
QY 313 SADIVLVTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIROGK 372
Db 256 EAKYVISAIPPTLGMKIHFNPPLPMRNQMITRVLPGSVIKVICVYKPFWRKKDY-CGT 314
QY 373 SITDGPRIYIY-----PSHSFHTNETIGVLLASYTWSDESLLPLGASDEBELKEL--- 422
Db 315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHKARKLARL-----TKEERLKKLCBLY 368
QY 423 -----ALRDLAKIHGEQVWDKCTGVIVKWSADPYSGLGAFALFTPYOHL-EYAQELFSSE 476
Db 369 AKVLGSLALEPVHYEE-----KNWCEEQYSGGCYTTYPFPGLTQYGRVLRQPV 418
QY 477 GRVHFAGEHTAPPH--AWIETSMKSAIRAATNI----NKVANE 514
Db 419 DRIYFAGTETA--THWSGYMEGAVEAGERAAREILHAMGKIPED 461

RESULT 11
US-10-990-328A-8288
; Sequence 8288, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8288
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-990-328A-8288

Query Match      10.7%; Score 288; DB 6; Length 520;
Best Local Similarity 25.0%; Pred. No. 5.4e-13;
Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;

QY 62 VVIVAGMAGLTAAKLLDAGHTVTLLEANDRVGGRVETYNKEGWAEGMAMRI-PSS 120
Db 7 VVVVGGSIGMAAKLLHDSGLNVVLEARDRVGGRTYTLRNQKVK-YVDLGGSYVGPTQ 65
QY 121 HRIVQMFVKKLGV---MNEFVMTDDNTFYLVNGVRERTYVQE-----NPDVLKYNVS 171
Db 66 NRILR-LAKELGLETYKNEVER-----LIHHVKGKSYPRGPPVWNP--ITY--- 112
QY 172 ESEKISADLLD-----RALQKVEEVEANG-CKAAL-EKYDRYSVKEYLKEEGLSPG 224
Db 113 -----LDHNNFWRTWDDMGREIPSDAPWKAPLAEWDNMTMKELL----- 152
QY 225 AVRMTGDLNQSMLYALTSEMIYDQADVDSVT--YHEVT----- 263
Db 153 -----DKLCWTESAKOL-ATLFVNLCVTAETHEVSALWFLVYVKQCGGTTIRIS 200
QY 264 -----GSDLLPEAFSLVDVPIILLNSKVKHQRSDKGVIVSYQTGNESLMDL 312
Db 201 TTNGQERKFGVGGQGVSEIRIMDLGDRVKLERPVYIDQRENVLV--ETLNHEM---Y 255
QY 313 SADIVLVTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIROGK 372
Db 256 EAKYVISAIPPTLGMKIHFNPPLPMRNQMITRVLPGSVIKVICVYKPFWRKKDY-CGT 314
QY 373 SITDGPRIYIY-----PSHSFHTNETIGVLLASYTWSDESLLPLGASDEBELKEL--- 422
Db 315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHKARKLARL-----TKEERLKKLCBLY 368
QY 423 -----ALRDLAKIHGEQVWDKCTGVIVKWSADPYSGLGAFALFTPYOHL-EYAQELFSSE 476
Db 369 AKVLGSLALEPVHYEE-----KNWCEEQYSGGCYTTYPFPGLTQYGRVLRQPV 418
QY 477 GRVHFAGEHTAPPH--AWIETSMKSAIRAATNI----NKVANE 514
Db 419 DRIYFAGTETA--THWSGYMEGAVEAGERAAREILHAMGKIPED 461

RESULT 12
US-11-051-454-252
; Sequence 252, Application US/11051454
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/11/051,454
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-09248-11

Query Match      10.5%; Score 283; DB 1; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.3e-12;
Matches 121; Conservative 91; Mismatches 197; Indels 108; Gaps 18

Qy 62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRUGRGVETYNKEGHYAEMGARIPSSH 121
   ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
Db 16 VVWIGGGISGLSAKLLTEYGVSVLLEARDRVGRGTYYTIRNEHVDYDVVGGA VGPQN 75

Qy 122 RIVOWFKVLGVENVEFWMTDDNTFYLVNGVRETYVQE-----NP-DVLKNVSESE 174
   ||::||::||::||::||::||::||::||::||::||::||::||::||
Db 76 RLRL-LSELGLGIETYKYNVSE---RLVQVKGKTYPFRCGAFPPVMNPIAYLDYN----- 125

Qy 175 KGISADLLRALQKVKEEVEANGCKAA--LEKYDRYSVKLEYLKEEGLSPGAVRMIGDL 232
   ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
Db 126 -----NLWRITDNMGKEIPTDPAPWAQAHAQKWDKWTMB-----L 160

Qy 233 LNEOSLMYTALSEMICYDAQNDVSITYHEVT----- 263
   :::::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
Db 161 IDKICWTKTA-RRFAYLFVNINVTSEPHEVSALWFLWVVKQCQTTRIFSVTNQGQERKP 219

Qy 264 -GGSDDLPEAPLSVDLPVILLNKVKVHIROSDKGVIYSVOTGNESLMDSADILVTTT 322
   ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
Db 220 VGGSGQVSRIMDLLGDQVKLNHPVTHVDQSSDNIITE-TLNHEHYECKYVINAIPPTLT 278

Qy 323 AKAAALFDIDPPPLSISKWEALRSVHYDSSSTKILLTPRDKEWEDDGIRGKSITDGP SRYI 382
   |||||::||::||::||::||::||::||::||::||::||::||::||::||
Db 279 AK-----IHFPQLPAERNQLIQRLPMGAVTKMMYKBAFWKKDKYCGCMIIEDEDA PI- 333

Qy 383 YYPSPHSPTNET-----IGVLLASYTWSDBSLLFLGASDBELKELARLDL-AKHG 432
   ::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
Db 334 -----SITLDDTXPDGSLPALMGFILARK--ADR---LAKLHKRIKKKICELYAKVLG 382

Qy 433 EQWKDKCTGVIVKWSADPSYLGAP-ALFTPYQHLEYAQBELFSSEGRVHFAGEHTA---- 487
   ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
Db 383 SQBALHPVHYEEKNVCEEQYSGGCYTAFFPGIMTQYGRVIOPVGRIFPFAGTETATKWS 442

Qy 488 -FPHAMLETSMKSAIRAATNINKVANEEESTIEHTKOE 523
   ::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
Db 443 GYMGEAVEGERARAEREVLNGLGKVTBKDIWVOEPESK 479

RESULT 14
PCT-US03-10870-549
; Sequence 549, Application PC/TUS0310870
; GENERAL INFORMATION:
; APPLICANT: Mitokor, Inc.
; APPLICANT: Buck Institute
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fashy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; CURRENT APPLICATION NUMBER: PCT/US03/10870
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 549
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-10870-549

Query Match      10.5%; Score 283; DB 1; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.3e-12;
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 13:47:25 ; Search time 166 Seconds  
(without alignments)  
1220.858 Million cell updates/sec

Title: US-10-645-094-1  
Perfect score: 2703  
Sequence: 1 MNLHVWKLSVSVSLITLY.....TNINKVNESTIEHTKDEL 524

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	524	2	AAW96805
2	1048.5	38.8	523	8	ADO60382
3	1034	38.3	630	5	ABB10103
4	999	37.0	567	2	AAW75770
5	999	37.0	567	2	AAW06480
6	999	37.0	567	3	AAW93364
7	999	37.0	567	3	AAW93687
8	999	37.0	567	4	AAW66113
9	999	37.0	567	4	AAW72874
10	999	37.0	567	4	AAW50962
11	999	37.0	567	4	AAU12409
12	999	37.0	567	5	ABB84904
13	999	37.0	567	5	ABB10104
14	999	37.0	567	5	ABB95510
15	999	37.0	567	6	ABO17853
16	999	37.0	567	6	ADA56835
17	999	37.0	567	6	ABU81107
18	999	37.0	567	6	ABU71428
19	999	37.0	567	6	ABU66807
20	999	37.0	567	6	ADA40686
21	999	37.0	567	6	ABR47699
22	999	37.0	567	6	ABU59888
23	999	37.0	567	6	ABG74758
24	999	37.0	567	6	ABO25078
25	999	37.0	567	6	ABU67083

26	999	37.0	567	6	ADA45995	Ada45995	Novel hum
27	999	37.0	567	6	ADA76426	Ada76426	Human PRO
28	999	37.0	567	6	ADA19076	Ada19076	Human PRO
29	999	37.0	567	6	ADA61699	Ada61699	Homo sapi
30	999	37.0	567	6	ADB19484	ADB19484	Novel hum
31	999	37.0	567	6	ADB28025	ADB28025	Human PRO
32	999	37.0	567	6	ADA86504	ADA86504	Novel hum
33	999	37.0	567	6	ADB16068	ADB16068	Human PRO
34	999	37.0	567	6	ADA47854	Ada47854	Human PRO
35	999	37.0	567	6	ABO33606	ABO33606	Novel hum
36	999	37.0	567	6	ADA67649	Ada67649	Human PRO
37	999	37.0	567	6	ADB30656	ADB30656	Human PRO
38	999	37.0	567	6	ADA85952	ADA85952	Novel hum
39	999	37.0	567	6	ADA97164	Ada97164	Human PRO
40	999	37.0	567	6	ADA79468	Ada79468	Human PRO
41	999	37.0	567	6	ADA87607	Ada87607	Novel hum
42	999	37.0	567	6	ADB16809	ADB16809	Human PRO
43	999	37.0	567	6	ADA91901	Ada91901	Novel hum
44	999	37.0	567	6	ADB14964	ADB14964	Human PRO
45	999	37.0	567	6	ADB18925	ADB18925	Novel hum

## ALIGNMENTS

## RESULT 1

AAW96805  
ID AAW96805 standard; protein; 524 AA.

AC AAW96805;

DT 23-APR-1999 (first entry)

DE An apoptosis inducing protein.

XX Cell death; apoptosis; inhibition; proliferation; cancer cell;  
KW apoptosis inducing protein; AIP; chub mackerel; anticancer.

OS Scomber japonicus.

PN WO9852972-A1.

PD 26-NOV-1998.

PF 22-MAY-1998; 98WO-JP002261.

PR 23-MAY-1997; 97JP-00133549.

XX (TENS-) TENSEI SUISAN CO LTD.

XX Iwamoto M, Jung S;

DR WPI; 1999-070139/06.

DR N-ESDB; AAX15122.

PT Apoptosis inducing protein from mackerel and gene encoding it - for use

XX as anticancer agents.

PS Claim 1; Page 30-31; 47pp; Japanese.

CC The present sequence represents a protein which induces cell death  
(apoptosis) and inhibits the proliferation of cancer cells. The protein  
(apoptosis) inducing protein, AIP, is isolated from chub mackerel. The  
protein can be used as an anticancer agent and as a reagent for study of  
the mechanisms of apoptosis in vitro

XX Sequence 524 AA;

Query Match 100.0%; Score 2703; DB 2; Length 524;

Best Local Similarity 100.0%; Pred. No. 5.4e-206;

Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNLHVWKLSVSVSLITLYVSHVTLVALSLKHLADCLDKDYDTLLQTLQDNLGHPINTSH 60

1	Db		MNLFFVVKWKL	SVVSVLITL	YGGHTVALSL	KEHLADCE	DKDYD	LLQTLONG	PHINTSH	60
61	Qy		HVIVGAGMAGL	TAAKLLQDAGH	TVTILEANDR	VGGRVET	YRNEKEG	WYAE	GAMRIPSS	120
61	Db		HVIVGAGMAGL	TAAKLLQDAGH	TVTILEANDR	VGGRVET	YRNEKEG	WYAE	GAMRIPSS	120
121	Qy		HRIVQFVKKL	GVEMNEFV	MTDDNTFY	LNGVRBRT	VYVQEN	PDVLKYN	YSESEKISAD	180
121	Db		HRIVQFVKKL	GVEMNEFV	MTDDNTFY	LNGVRBRT	VYVQEN	PDVLKYN	YSESEKISAD	180
181	Qy		DLLDRLALQVK	VEVEANGC	KALEKXDR	YSKVEYI	KEEGGLS	PGAVRMI	GDLLEOSLMY	240
181	Db		DLLDRLALQVK	VEVEANGC	KALEKXDR	YSKVEYI	KEEGGLS	PGAVRMI	GDLLEOSLMY	240
241	Qy		TALSEMIYQD	AVNDSVT	VTHEVTG	SGDLLP	RAFLSV	LVDVPILL	NSKVKHIRQSD	300
241	Db		TALSEMIYQD	AVNDSVT	VTHEVTG	SGDLLP	RAFLSV	LVDVPILL	NSKVKHIRQSD	300
301	Qy		YQTGNESLMD	LSADIVL	VTTTAKAAL	FIDFDP	PLSIS	KMEALRS	VHYDSS	360
301	Db		YQTGNESLMD	LSADIVL	VTTTAKAAL	FIDFDP	PLSIS	KMEALRS	VHYDSS	360
361	Qy		KFWEDDGI	RGGKSI	TDGSPRI	YIYYP	SPSHSF	HNETIG	VULLASY	420
361	Db		KFWEDDGI	RGGKSI	TDGSPRI	YIYYP	SPSHSF	HNETIG	VULLASY	420
421	Qy		ELALRDLAKI	HGEQW	DKCTG	VIVVKW	SADP	YSLGAF	ALFTPYOHL	480
421	Db		ELALRDLAKI	HGEQW	DKCTG	VIVVKW	SADP	YSLGAF	ALFTPYOHL	480
481	Qy		FACEHTAF	PHAM	ETSMK	SAIRAA	TNINK	NKANE	ESTTIEHTKDEL	524
481	Db		FACEHTAF	PHAM	ETSMK	SAIRAA	TNINK	NKANE	ESTTIEHTKDEL	524

RESULT 2	
AD060382	
ID	AD060382 standard; protein; 523 AA.
XX	
AC	AD060382;
XX	
DT	15-JUL-2004 (first entry)
XX	
XX	Mouse L-amino acid oxidase protein seqID2.
DE	
XX	
KW	L-amino acid oxidase; antibacterial; antibacterial sterilisation;
KW	hydrogen peroxide supply component; bacterial infection;
KW	sexually transmitted disease; livestock; mastitis; antimicrobial; mouse;
KW	murine; enzyme.
XX	
OS	Mus sp.
XX	
PN	JP2004105119-A.
XX	
PD	08-APR-2004.
XX	
XX	19-SEP-2002; 2002JP-00274082.
PF	
XX	
PR	19-SEP-2002; 2002JP-00274082.
XX	
PA	(SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX	
XX	WPI; 2004-289536/27.
DR	N-PSDB; AD060381.
XX	
XX	
PT	Novel L-amino acid oxidase, useful in preparing antibacterial
PT	sterilization composition as hydrogen peroxide supply component which is
PT	useful for preventing, treating bacterial infection e.g. mastitis.
XX	
ES	Claim 2; SEQ ID NO 2; 46pp; Japanese.
XX	
CC	This invention relates to a novel protein having 27-523 amino acids of L

CC	amino acid oxidase having a fully defined amino acid sequence of 523
CC	amino acids as given in the specification and L-amino acid oxidase
CC	activity. The invention may be useful for the production of compounds
CC	with an antibacterial activity. The invention is useful in preparing an
CC	antibacterial sterilisation composition as a hydrogen peroxide supply
CC	component. The invention is useful for preventing, treating bacterial
CC	infections such as sexually transmitted disease in the breast of
CC	livestock, for example mastitis, and provides an antimicrobial effect.
CC	The present sequence is that of the mouse L-amino acid oxidase protein of
CC	the invention.
XX	
SO	Sequence 523 AA;
	Query Match
	Best Local Similarity 38.8%; Score 1048.5; DB 8; Length 523;
	Matches 226; Conservative 79; Mismatches 166; Indels 49; Gaps 7;
Qy	27 LSLKEHLADCLDEKDYDTLLQTLDNGLPHINTSHHVIVVIGMAGLTAAKLLQDAGHTVT 86
Db	25 LALYENLVKCFQDPDYEAFLIIAQNGLHTSPLSKRVVVVVGAGMAGLVAAKTLQDAGHEVT 84
Qy	87 ILEANDRVGRVETRYNEKEGWAEMGAMRIIPSSHRIVQWFKVLGVEMNEFVMTDDNTF 146
Db	85 ILEASNHIGGRVTVLRNKEBGWLELGPMPRIPESHKLIHTVYQKLGKLNKFNQYDSNTW 144
Qy	147 YLVNGVRETVVOENPDVLKYNVSESEKGISADDLLDRALQKVKEEVEANGCKAALEKY 206
Db	145 YLLNGQYRASEVMANFGILGYLPSPKONKVTVDLFVQAATKIKPHRKTSCNSQLLSLY 204
Qy	207 DRYSVKEYLKEBGLSPGAVRMIGDLNLEQSLMTALSEMIYDQADVNDVVT--YHEVTG 264
Db	205 DSYSTKAYLMKEGTLKRAHR-----DDRGYNDENAGYKSLIG 243
Qy	265 GSD-----LLPEAFL-----SVLDVPILLNSKVKHIRQSDKGVIVSYOT- 303
Db	244 VSECKHLLQKCPFRDHRWLCPIPNGLSASLKPGTIRLMSKVRVVDGPKVKVMYRTD 303
Qy	304 GNESLLMDLSADIVLVTTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRDKFW 363
Db	304 GPISALHKLADYAVIITASAKATLITFPPLSPREKTHALRSVHYTSATKVVLVCNERFW 363
Qy	364 EDGIRGKGIITGQPSYIYYPHSFHTNETIGVLLASYSWDSLSLPLGASDELKELA 423
Db	364 EQDGIRGGYSITDRPSRFIYYPHSLSLPGGK--GVLLASFTVGDDSSFFAALKPNQVVDV 421
Qy	424 LRDLAKTH--GEQWDKCTGVIVKWSADPYSYGAFALFPYQHLVAYQELFSSEGRVH 480
Db	422 LDDLAAVHRIPKEELKMKCPKSAIKHWSLDPLTIGAFTEFTFYOFVDYSKOLSPGEGRIY 481
Qy	481 FAGEHTAPPAHWIETSMKSAIRAATNTNKVANEESTIEHT 520
Db	482 FAGEHTCLPSHWIDTAIKSGIRASCNQAADVKEATRGHT 521
RESULT 3	
ABB10103	
ID	ABB10103 standard; protein; 630 AA.
XX	
AC	ABB10103;
XX	
DT	01-JUL-2002 (first entry)
XX	
DE	Mouse immediate early interleukin-four induced protein.
KW	Interleukin-four induced protein; IL-4; cytostatic; antifungal;
KW	antibacterial; immunomodulator; antiinflammatory; dermatological;
KW	immunosuppressive; immune disease; tumour; fungal infection;
KW	bacterial infection; systemic lupus erythematosus;
KW	inflammatory bowel disease; Guillain-Barre syndrome; Whipple's disease;
KW	atopic dermatitis; food hypersensitivity; rheumatoid arthritis;
KW	osteoarthritis; diabetes mellitus; psoriasis; gene therapy; mouse.
XX	
OS	Mus sp.



CC translation product does not have the key residues which covalently bind  
CC the FAD cofactor, and so may not exhibit monoamine oxidase activity. The  
CC cellular types which express messages encoding YTF03 suggest that signals  
CC important in cell differentiation and development are mediated by them.  
CC The invention provides a process for recombinant production of YTF03,  
CC host cells, expression vectors and specific antibodies. The products can  
CC be used for detection, diagnosis, development of therapeutic methods and  
CC drug screening  
XX  
XX Sequence 567 AA;

Query Match 37.0%; Score 999; DB 2; Length 567;  
Best Local Similarity 41.8%; Pred. No. 1.8e-70;  
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVWVKLSVSVLITLYSHT-VALSLKEHLADCLEDKDYDTLLQTLNDGLPHINTSHH 61  
DB 6 LHL-----LVLVPIILLSVASQDWKAERSQDPPEKCMQDPDYEQLLKVVTVGLNRTLPQR 61  
QY 62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRVGGRVETRYNEKEGVAEMGAMRIPSSH 121  
DB 62 VIVVGAGVAGLVAALKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIIGELGAMRMPSSH 121  
QY 122 RIVQWFVKLGVEMNEFVMTDNTFYLVNGVRRTYVVOENPDVLKYNVSESEKIGISADD 181  
DB 122 RILHLKCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVVEKVPKLGVALRPOEKHSPED 181  
QY 182 LLDRALQKVEEVEANGCKAALEKDYRSVKYKEEGLSPGAVRMIGLLNEQSLMYT 241  
DB 182 IYQWALNQALKDLKALGCRKAMKFFERTLLEVLGEGNLSRPAVQLLDVMSDGGFFYL 241  
QY 242 ALSEMIYDQADVNDSTVYHEVTGSDLLPEAFLSVLDVPIILNSKVKHROSQDKGIVISY 301  
DB 242 SFAEALRAHSCLSDRLOYSRIVGGWDLPLRALLSLSGLVLLNAPVAMTQCPHDVHQI 301  
QY 302 QTGNES-SLMDLSADIVLVTAKAALFDIDPPPLSISKWEALRSVHDSSTKILLTPRD 360  
DB 302 ETPSPARNLKVLDKADVLLTASGPVAKRITFPPLRHMQEARLRLHYVPATKVPFLSPRR 361  
QY 361 KFWEDDGRGKSIIDGPRYIYIPSHSPHTWETIGVLLASVTWSDSILLFISASDEELK 420  
DB 362 PFWREHIEGHSNTRDSRMIFYP-----PPREGALLASTWSDAAAFAAGLSREAL 416  
QY 421 ELALDLAKIHG---EQWMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476  
DB 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGFVQPP-----ALWQTEK 466  
QY 477 -----GRVHFAGETAFPHAWITSMKSAIRAATNIN 508  
DB 467 DDMTVPYGRIFYPAGEHTAYPHGWVETAVKSALRAAIAKIN 505

RESULT 5  
ID AAY06480  
XX AAY06480 standard; protein; 567 AA.  
XX AC AAY06480;  
XX DT 27-SEP-1999 (first entry)  
XX DE Human tumour-associated protein PRO1265.  
XX KW PRO1265; UNQ636; cancer; tumour; diagnosis; therapy; human.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Peptide 1..21  
FT /note= "signal peptide"  
FT Protein 22..567  
FT /note= "mature protein"  
FT Modified-site 54..57  
FT /note= "Asn is N-glycosylated"

FT Region 61..80  
FT /note= "homology to D-amino acid oxidase"  
FT Modified-site 134..137  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 220..223  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 559..562  
FT /note= "Asn is N-glycosylated"  
XX  
XX WO9935170-A2.  
XX  
XX 15-JUL-1999.  
XX  
XX 05-JAN-1999; 99WO-US000106.  
XX  
XX 05-JAN-1998; 98US-0070440P.  
XX 29-APR-1998; 98US-0083500P.  
XX 22-MAY-1998; 98US-0086414P.  
XX 10-JUN-1998; 98US-0088742P.  
XX 10-NOV-1998; 98US-0107783P.  
XX 20-NOV-1998; 98US-0109304P.  
XX (GETH ) GENENTECH INC.  
XX  
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;  
XX Wood WT;  
XX  
XX WPI; 1999-430385/36.  
XX N-PSDB; AAX87257.  
XX  
XX Antibody against proteins expressed in neoplastic cells, useful for tumor  
XX diagnosis and treatment.  
XX  
XX Example 1; Fig 8; 162pp; English.

XX This sequence represents human PRO1265 (UNQ636), a 62.9 kDa protein (pI  
XX 8.97) encoded by the novel cDNA clone DNA60764 (see AAX87257).  
XX Amplification of DNA60764 occurs in various lung and colon tumours and  
XX cell lines, suggesting a significant role in tumour formation and growth.  
XX Antagonists (e.g. antibodies) directed to PRO1265 may have use in cancer  
XX therapy. The invention identifies 14 genes (see AAX87254-67) that are  
XX amplified in the genome of tumour cells. Such amplification is expected  
XX to be associated with overexpression of the gene product and to  
XX contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may  
XX be useful targets for the diagnosis and/or treatment (including  
XX prevention) of certain cancers, and may act as predictors of the  
XX prognosis of tumour treatment. Antibodies that bind the proteins are  
XX claimed and used in claimed cancer diagnostic kits  
XX  
XX Sequence 567 AA;

Query Match 37.0%; Score 999; DB 2; Length 567;  
Best Local Similarity 41.8%; Pred. No. 1.8e-70;  
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVWVKLSVSVLITLYSHT-VALSLKEHLADCLEDKDYDTLLQTLNDGLPHINTSHH 61  
DB 6 LHL-----LVLVPIILLSVASQDWKAERSQDPPEKCMQDPDYEQLLKVVTVGLNRTLPQR 61  
QY 62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRVGGRVETRYNEKEGVAEMGAMRIPSSH 121  
DB 62 VIVVGAGVAGLVAALKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIIGELGAMRMPSSH 121  
QY 122 RIVQWFVKLGVEMNEFVMTDNTFYLVNGVRRTYVVOENPDVLKYNVSESEKIGISADD 181  
DB 122 RILHLKCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVVEKVPKLGVALRPOEKHSPED 181  
QY 182 LLDRALQKVEEVEANGCKAALEKDYRSVKYKEEGLSPGAVRMIGLLNEQSLMYT 241  
DB 182 IYQWALNQALKDLKALGCRKAMKFFERTLLEVLGEGNLSRPAVQLLDVMSDGGFFYL 241  
QY 242 ALSEMIYDQADVNDSTVYHEVTGSDLLPEAFLSVLDVPIILNSKVKHROSQDKGIVISY 301  
DB 242 SFAEALRAHSCLSDRLOYSRIVGGWDLPLRALLSLSGLVLLNAPVAMTQCPHDVHQI 301

Db	242	SFAEALRAHSCLSDBLQYSRIVGGWDLPLPRALLSSLSGLVLNAPVAMTQGPDPHVHVOI	301	PR	18-SEP-1998;	98US-0100848P.
Oy	302	QTGNES-SLMDLSADIVLTTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTRFD	360	PR	18-SEP-1998;	98US-0100849P.
Db	302	ETSPPARNLKVLKADVLLTAGSPAVKRTITFSPPLPRHQEALRLHYVPATKVLFSFR	361	PR	18-SEP-1998;	98US-0101068P.
Oy	361	KWEDDGTGRGKSITDGSRYIYYPSHSFHTNETIGVLLASTWDSLSLLFLGASDEBLK	420	PR	22-SEP-1998;	98US-0101071P.
Db	362	PFWREHEGGHSNDRPSRMIFYP-----PPREGALLIASYTSDAAAAFAGLSREBAL	416	PR	23-SEP-1998;	98US-0101279P.
Oy	421	ELALRDLAKING---EQWMDKCTGIVVKWSADPYSLGAFAFLFTPYQHLEVAQELFSSE-	476	PR	23-SEP-1998;	98US-0101471P.
Db	417	RLALDDVAALHGPPVRQWLDG-TGV-VKRWEDQHSQGFVVQPP-----ALWQTEK	466	PR	23-SEP-1998;	98US-0101472P.
Oy	477	-----GRVHPAGSHTAFFPAWIETSMKSAIRAATNIN 508		PR	23-SEP-1998;	98US-0101475P.
Db	467	DDWTPVYGRIFYAGEHTAYPHGWVETAVKSALRAAIKIN 505		PR	23-SEP-1998;	98US-0101476P.
RESULT 6				PR	23-SEP-1998;	98US-0101477P.
AA993364				PR	24-SEP-1998;	98US-0101741P.
ID	AA993364	standard; protein; 567 AA.		PR	24-SEP-1998;	98US-0101743P.
XX	AC	AA993364;		PR	24-SEP-1998;	98US-0101915P.
XX	DT	08-AUG-2000 (first entry)		PR	24-SEP-1998;	98US-0101916P.
XX	DE	Human PRO1265 (UNQ636) amino acid sequence SEQ ID NO:84.		PR	29-SEP-1998;	98US-0102207P.
XX	DE	Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;		PR	29-SEP-1998;	98US-0102307P.
KW	transmembrane; secretion; immunoadhesion; pharmaceutical; screening.			PR	29-SEP-1998;	98US-0102330P.
XX	OS	Homo sapiens.		PR	29-SEP-1998;	98US-0102331P.
XX	PN	WO200012708-A2.		PR	30-SEP-1998;	98US-0102484P.
XX	PD	09-MAR-2000.		PR	30-SEP-1998;	98US-0102570P.
XX	PF	01-SEP-1999; 99WO-US020111.		PR	30-SEP-1998;	98US-0102487P.
XX	PR	01-SEP-1998; 98US-0098716P.		PR	01-OCT-1998;	98US-0102684P.
PR	01-SEP-1998;	98US-0098749P.		PR	02-OCT-1998;	98US-0102687P.
PR	02-SEP-1998;	98US-0098803P.		PR	06-OCT-1998;	98US-0102965P.
PR	02-SEP-1998;	98US-0098821P.		PR	06-OCT-1998;	98US-0103258P.
PR	02-SEP-1998;	98US-0098843P.		PR	07-OCT-1998;	98US-0103449P.
PR	09-SEP-1998;	98US-0098538P.		PR	07-OCT-1998;	98US-0103314P.
PR	09-SEP-1998;	98US-0099596P.		PR	07-OCT-1998;	98US-0103315P.
PR	09-SEP-1998;	98US-0099602P.		PR	07-OCT-1998;	98US-0103328P.
PR	09-SEP-1998;	98US-0099642P.		PR	08-OCT-1998;	98US-0103359P.
PR	10-SEP-1998;	98US-0099741P.		PR	08-OCT-1998;	98US-0103401P.
PR	10-SEP-1998;	98US-0099754P.		PR	08-OCT-1998;	98US-0103678P.
PR	10-SEP-1998;	98US-0099763P.		PR	08-OCT-1998;	98US-0103679P.
PR	10-SEP-1998;	98US-0099792P.		PR	14-OCT-1998;	98US-0103711P.
PR	10-SEP-1998;	98US-0099808P.		PR	20-OCT-1998;	98US-0104257P.
PR	10-SEP-1998;	98US-009812P.		PR	20-OCT-1998;	98US-0104987P.
PR	10-SEP-1998;	98US-009815P.		PR	20-OCT-1998;	98US-0105000P.
PR	10-SEP-1998;	98US-009818P.		PR	21-OCT-1998;	98US-0105002P.
PR	15-SEP-1998;	98US-0100388P.		PR	22-OCT-1998;	98US-0105104P.
PR	15-SEP-1998;	98US-0100390P.		PR	22-OCT-1998;	98US-0105169P.
PR	16-SEP-1998;	98US-0100584P.		PR	26-OCT-1998;	98US-0105266P.
PR	16-SEP-1998;	98US-0100627P.		PR	26-OCT-1998;	98US-0105693P.
PR	16-SEP-1998;	98US-0100661P.		PR	27-OCT-1998;	98US-0105694P.
PR	16-SEP-1998;	98US-0100662P.		PR	27-OCT-1998;	98US-0105807P.
PR	16-SEP-1998;	98US-0100664P.		PR	27-OCT-1998;	98US-0105881P.
PR	17-SEP-1998;	98US-0100683P.		PR	27-OCT-1998;	98US-0105882P.
PR	17-SEP-1998;	98US-0100684P.		PR	28-OCT-1998;	98US-0106023P.
PR	17-SEP-1998;	98US-0100710P.		PR	28-OCT-1998;	98US-0106024P.
PR	17-SEP-1998;	98US-0100711P.		PR	28-OCT-1998;	98US-0106032P.
PR	17-SEP-1998;	98US-0100919P.		PR	28-OCT-1998;	98US-0106033P.
PR	17-SEP-1998;	98US-0100930P.		PR	29-OCT-1998;	98US-0106178P.
PR	17-SEP-1998;	98US-0100932P.		PR	29-OCT-1998;	98US-0106248P.
PR	17-SEP-1998;	98US-0100933P.		PR	29-OCT-1998;	98US-0106384P.
PR	17-SEP-1998;	98US-0100934P.		PR	29-OCT-1998;	98US-0106500P.
PR	17-SEP-1998;	98US-0100935P.		PR	30-OCT-1998;	98US-0106464P.
PR	17-SEP-1998;	98US-0100936P.		PR	03-NOV-1998;	98US-0106856P.
PR	17-SEP-1998;	98US-0100937P.		PR	03-NOV-1998;	98US-0106902P.
PR	17-SEP-1998;	98US-0100938P.		PR	03-NOV-1998;	98US-0106905P.
PR	17-SEP-1998;	98US-0100939P.		PR	03-NOV-1998;	98US-0106919P.
PR	17-SEP-1998;	98US-0100940P.		PR	03-NOV-1998;	98US-0106932P.
PR	17-SEP-1998;	98US-0100941P.		PR	03-NOV-1998;	98US-0106934P.
PR	17-SEP-1998;	98US-0100942P.		PR	17-NOV-1998;	98US-0107783P.
PR	17-SEP-1998;	98US-0100943P.		PR	17-NOV-1998;	98US-0108775P.



PS Claim 61; Fig 8; 220pp; English.

XX The present sequence represents a novel human polypeptide. The

CC specification describes novel polypeptides designated PRO201, PRO292,

CC PRO327, PRO1265, PRO344, PRO347, PRO357, PRO715, PRO1017, the

CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the

CC genome of tumour cells. The polypeptides are believed to contribute to

CC tumourigenesis. The polypeptides are useful target for the identification

CC of certain cancers, and may act as predictors of the prognosis of tumour

CC treatment. Antibodies against these polypeptides are useful in the

CC treatment and diagnosis of neoplastic cell growth and proliferation in

CC mammals

XX Sequence 567 AA;

SQ

Query Match 37.0%; Score 999; DB 3; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.8e-70;

Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVVKWKLVSIVLITLYYSHT-VALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSHH 61

DB 6 LHL-----LVLVPIILLSVASODWKAERSQDPFEKCMQDPDYEQLLKVVTVGLNRLTKPOR 61

QY 62 VVIVGAGVAGLTAALKLQDAGHTVTILEANDRVGRVETRYNEKEGVAEMGAMRIPSSH 121

DB 62 VVIVGAGVAGLVAAKVLS DAGHKVTILEADNRIGRIFTYRDQNTGWIGELGAMRMPSSH 121

QY 122 RIVQWFKVKGVEEMNEFVMTDNTFYLVNGVRERTYVVOENPDVLKYNVSEKGISADD 181

DB 122 RILHLKCOGLNLTKFTQYDKNTWTVEHVKLRNVYVEKVPKLGVALRPOEKHSPED 181

QY 182 LLDRLALQVKVEEVANGKAALEKYDYSVKEYLKEEGSLSPGAVRMIGDLNLSQSLMYT 241

DB 182 IQVMALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLDVNSEGFFYL 241

QY 242 ALSEMIYQDADVNDVSVTHVETGSDLLPEAFSLVDVPIILNSKVYHIROSDKGVIVSY 301

DB 242 SFAELRAHSCLSDRLOYSRIVGGWDLPLRALLSSLSGLVLNAPVAVMTQGPVHVQI 301

QY 302 QTGNES-SLMDLSADIVLVTTTAKAALFIDFDPPLISIKMBALRSVHYDSSTKILLTPRD 360

DB 302 ETSPPARNLKVLDKADVLLTASGPAVKRITFSPPLPRHMQEALRLHLYVPATKVFSPFR 361

QY 361 KFWEDDGIKGGKSIIDGPSRIYYPSPHSFHTNETIGVLLASVTWSDLSLLFLGASDEELK 420

DB 362 PWREEHIEGHSNTDRPSRMIFYP-----PPREGALLASTYTWSDAAAFAAGLSREAL 416

QY 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGVVQPP-----ALWQTEK 466

QY 477 -----GRVHPAGEHTAPPHAWITSMKSAIRAATNIN 508

DB 467 DDMVTVPYGRIVPAGEHTAYPHGWVETAVKSAIRAAIKIN 505

RESULT 8

ID AAB66113

XX AAB66113 standard; protein; 567 AA.

XX AAB66113;

AC

XX 02-APR-2001 (first entry)

DT

XX Protein of the invention #25.

DE

XX Secreted; transmembrane; gene therapy.

KW

XX Unidentified.

OS

XX WO200078961-A1.

PN

XX 28-DEC-2000.

PD

XX 18-FEB-2000; 2000WO-US004342.

PF

XX 23-JUN-1999; 99US-0141037P.

PR

XX 20-JUL-1999; 99US-0144758P.

PR

XX 26-JUL-1999; 99US-0145698P.

PR

XX 01-SEP-1999; 99WO-US020111.

PR

XX 29-OCT-1999; 99US-0162506P.

PR

XX 30-NOV-1999; 99WO-US028313.

PR

XX 02-DEC-1999; 99WO-US028551.

PR

XX 16-DEC-1999; 99WO-US030095.

PR

XX 05-JAN-2000; 2000WO-US000219.

PR

XX 06-JAN-2000; 2000WO-US000376.

XX

PA (GETH ) GENENTECH INC.

XX

XX Baker KP, Botstein D, Deenoyers L, Eaton DL, Ferrara N, Fong S,

PI

PI Gao W, Goddard A, Godowski FJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI

PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;

PI

PI Williams PM, Wood WI;

XX

XX WPI; 2001-071395/08.

DR

XX Secreted and transmembrane proteins and nucleic acids designated PRO,

PT

PT useful as hybridization probes, in chromosome and gene mapping and gene

PT

PT therapy.

XX

XX Claim 1; Fig 50; 787pp; English.

PS

XX The present invention relates to secreted and transmembrane proteins.

CC

CC These proteins and the DNA encoding them may be used as hybridization

CC

CC probes, in chromosome and gene mapping and in the generation of anti-

CC

CC sense RNA and DNA. They may also be used to generate either

CC

CC transgenic animals or knockout animals which are in turn useful for

CC

CC development and screening of therapeutically useful reagents. The nucleic

CC

CC acids may also be used in gene therapy

XX

XX Sequence 567 AA;

SQ

Query Match 37.0%; Score 999; DB 4; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.8e-70;

Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVVKWKLVSIVLITLYYSHT-VALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSHH 61

DB 6 LHL-----LVLVPIILLSVASODWKAERSQDPFEKCMQDPDYEQLLKVVTVGLNRLTKPOR 61

QY 62 VVIVGAGVAGLTAALKLQDAGHTVTILEANDRVGRVETRYNEKEGVAEMGAMRIPSSH 121

DB 62 VVIVGAGVAGLVAAKVLS DAGHKVTILEADNRIGRIFTYRDQNTGWIGELGAMRMPSSH 121

QY 122 RIVQWFKVKGVEEMNEFVMTDNTFYLVNGVRERTYVVOENPDVLKYNVSEKGISADD 181

DB 122 RILHLKCOGLNLTKFTQYDKNTWTVEHVKLRNVYVEKVPKLGVALRPOEKHSPED 181

QY 182 LLDRLALQVKVEEVANGKAALEKYDYSVKEYLKEEGSLSPGAVRMIGDLNLSQSLMYT 241

DB 182 IQVMALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLDVNSEGFFYL 241

QY 242 ALSEMIYQDADVNDVSVTHVETGSDLLPEAFSLVDVPIILNSKVYHIROSDKGVIVSY 301

DB 242 SFAELRAHSCLSDRLOYSRIVGGWDLPLRALLSSLSGLVLNAPVAVMTQGPVHVQI 301

QY 302 QTGNES-SLMDLSADIVLVTTTAKAALFIDFDPPLISIKMBALRSVHYDSSTKILLTPRD 360

DB 302 ETSPPARNLKVLDKADVLLTASGPAVKRITFSPPLPRHMQEALRLHLYVPATKVFSPFR 361

QY 361 KFWEDDGIKGGKSIIDGPSRIYYPSPHSFHTNETIGVLLASVTWSDLSLLFLGASDEELK 420

DB 362 PWREEHIEGHSNTDRPSRMIFYP-----PPREGALLASTYTWSDAAAFAAGLSREAL 416

QY 421 ELALRDLAKIHG---EQWMDKCTGIVVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476

DB 421 ELALRDLAKIHG---EQWMDKCTGIVVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476

Db 417 RLALDDVAALHGVVVRQLWDG-TGV-VKRWABDQHSQGGFVVQPP-----ALWQTEK 466

Qy 477 -----GRVHPAGHTAFPHAWIETSMKSATRAATNIN 508

Db 467 DDMVTVPYGRIFYPAGEHTAYPHGWVETAVKSALRAAIKIN 505

RESULT 9

AA72874

ID AAY72874 standard; protein; 567 AA.

XX

AC AAY72874;

XX 31-MAY-2001 (first entry)

XX Human PRO1265 protein encoded by DNA60764-1533 cDNA clone.

XX Human; PRO1265; antiinflammatory; dermatological; immunosuppressive;  
 KW antirheumatic; antiarthritic; osteopathic; antianaemic; haemostatic;  
 KW antithyroid; antidiabetic; antiviral; antipsoriatic; antiallergic;  
 KW antiasthmatic; inhibitor; therapy; systemic lupus erythematosus;  
 KW spondyloarthropathy; systemic sclerosis; systemic vasculitis;  
 KW sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome;  
 KW autoimmune thrombocytopenia; immune-mediated renal disease; hepatitis;  
 KW demyelinating polyneuropathy; Guillain-Barre syndrome; Whipple's disease;  
 KW hepatobiliary disease; primary biliary cirrhosis; sclerosing cholangitis;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy; skin disease;  
 KW allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria;  
 KW eosinophilic pneumonia; hypersensitivity pneumonitis; graft rejection;  
 KW idiopathic pulmonary fibrosis; graft-versus-host-disease.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21 /label= Signal\_peptide

FT Protein 22..567

FT Modified-site 35..43 /label= Mature\_human\_PRO1265\_protein

FT Modified-site 52..58 /label= Tyrosine\_kinase\_phosphorylation\_site

FT Modified-site 54..58 /note= "N-myristoylation site"

FT Region 61..81 /note= "Asn is N-glycosylated"

FT Modified-site 66..74 /label= D-amino\_acid\_oxidase\_protein

FT Modified-site 71..77 /note= "N-myristoylation site"

FT Modified-site 130..136 /note= "N-myristoylation site"

FT Modified-site 132..138 /note= "N-myristoylation site"

FT Modified-site 134..138 /note= "Asn is N-glycosylated"

FT Modified-site 161..169 /label= Tyrosine\_kinase\_phosphorylation\_site

FT Modified-site 198..204 /note= "N-myristoylation site"

FT Modified-site 220..224 /note= "Asn is N-glycosylated"

FT Modified-site 371..377 /note= "N-myristoylation site"

FT Modified-site 559..563 /note= "Asn is N-glycosylated"

XX WO200116319-A2.

XX 08-MAR-2001.

XX 23-AUG-2000; 2000WO-US023522.

XX

PR 31-AUG-1999; 99US-0151733P.

PR 01-SEP-1999; 99WO-US020111.

PR 16-DEC-1999; 99WO-US030095.

PR 18-FEB-2000; 2000WO-US004342.

PR 01-MAR-2000; 2000WO-US005601.

PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 05-JUN-2000; 2000US-0209832P.

XX (GETH ) GENENTECH INC.

XX Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Tumas D;

PI Watanabe CK, Wood WI;

XX WPI; 2001-226690/23.

DR N-PSDB; AAD02920.

XX New PRO polypeptides for treating immune related and inflammatory

PT diseases such as rheumatoid arthritis, systemic vasculitis, asthma,

PT autoimmune hemolytic anemia, and diabetes mellitus.

XX Claim 10; Fig 2; 119pp; English.

XX The present sequence is PRO1265 protein encoded by DNA60764-1533 cDNA

CC clone. PRO protein, its agonist or antagonist or its antibody which are

CC capable of enhancing or inhibiting the proliferation of T-lymphocytes or

CC of increasing the infiltration of inflammatory cells into a tissue are

CC mammals. The PRO protein is useful for treating systemic lupus

CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic

CC inflammatory myopathy, Sjogren's syndrome, systemic sclerosis, idiopathic

CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia,

CC thyroiditis, diabetes mellitus, immune-mediated renal disease,

CC demyelinating disease of the central or peripheral nervous system,

CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic

CC inflammatory demyelinating polyneuropathy, hepatobiliary disease,

CC infectious or autoimmune chronic active hepatitis, primary biliary

CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory

CC bowel disease, gluten-sensitive enteropathy, Whipple's disease,

CC autoimmune or immune-mediated skin diseases such as bullous skin disease,

CC erythema multiforme and contact dermatitis, psoriasis, allergic diseases

CC such as asthma, allergic rhinitis, atopic dermatitis, food

CC hypersensitivity and urticaria, immunologic diseases of the lung such as

CC eosinophilic pneumonias, idiopathic pulmonary fibrosis, hyper-

CC sensitivity pneumonitis, transplantation associated diseases such as

CC graft rejection or graft-versus-host-disease

XX SQ Sequence 567 AA;

XX Query Match 37.0%; Score 999; DB 4; Length 567;

XX Best Local Similarity 41.8%; Pred. No. 1.8e-70;

XX Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVVKWKLVSIVLITLYSHT-VALSLKHLADCLEDKDYDTLQTLQDNLGPHINTSHH 61

Db 6 LHL-----LVIVPILLSVASQDWKAERSQDFEKCQMDPYEQLLKVVTVGLNRTLKQQR 61

Qy 62 VVIVGAGNAGLTAAKLQDAGHTVTTLLEANDRVGGRVETTYRNEKEGWAENGAMRIPSSH 121

Db 62 VIVVGAGVAGLVAARKVLSLDAGHKVTILEADNRIGRIFTYRDQNTQGTGELGAMRPSH 121

Qy 122 RIVQMFVKLGVENNEFVMTDNTFYLVNGVRETYVVOENPDVLKVNVSSEKISADD 181

Db 122 RILHLKCOGLGLNLTQYDKNTWTEVHEVKLRNVVVEKPEKLGVALRPOEKHSPED 181

Qy 182 LLDRLAQVKEEVEANGCKAALEKYDYSVKEYLKEEGGLSPGAVRMICDLINEOSLMYT 241

Db 182 IYQVALNQALKDLKALGCRKAMKFERHTLLYLLGEGNLSPAPVQLLGDVMSDEGFFYL 241

Qy 242 ALSEMIYDQADVNDSTVTHEVTGSGDDLPEAFLSVLDPILLNSKVKHROSQKGVISY 301

Db 242 SFAEALRAHSCUSDRLOYSRIYGVGGWDLPRALLSSGLVLLNAPVAVMTQGHVDHVQI 301  
Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTRPD 360  
Db 302 ETSPPARNLKVLKADVLLTASGPAVKRITFSPPLPRHMQEALRLHYVPATKVFLSFR 361  
Qy 361 KFWEDDGIRGKSIITDGPRIYYPSSHFTNETIGVLLASYTWSDESLLFLGASDEELK 420  
Db 362 PFWEHEHIEGHSNTDRPSRMIFYP-----PPREGALLASYTWSDAFAAGLSREEL 416  
Qy 421 ELALRDLAKIHG---EQVMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSP- 476  
Db 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALWQTEK 466  
Qy 477 -----GRVHFAGETHAPPHAWIETSMKSIRAATNIN 508  
Db 467 DDWTPVYGRYIYFAGEHTAYPHGWVETAVKSALRAAIKIN 505

RESULT 10  
AAB50962  
ID AAB50962 standard; protein; 567 AA.

XX AAB50962;  
DT 21-MAR-2001 (first entry)  
XX Human PRO1265 protein.  
XX Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;  
KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;  
KW PRO agonist; cancer; inflammatory disorder; immunological disorder.  
XX Homo sapiens.  
XX WO200073348-A2.  
XX 07-DEC-2000.  
XX 30-MAY-2000; 2000WO-US014941.  
XX 02-JUN-1999; 99WO-US012252.  
XX 22-JUN-1999; 99US-0140650P.  
XX 23-JUN-1999; 99US-0141037P.  
XX 20-JUL-1999; 99US-0144758P.  
XX 01-SEP-1999; 99WO-US020111.  
XX 08-SEP-1999; 99WO-US020594.  
XX 29-OCT-1999; 99US-0162506P.  
XX 30-NOV-1999; 99WO-US028313.  
XX 01-DEC-1999; 99WO-US028634.  
XX 02-DEC-1999; 99WO-US028551.  
XX 09-DEC-1999; 99US-0170262P.  
XX 16-DEC-1999; 99WO-US030095.  
XX 20-DEC-1999; 99WO-US030999.  
XX 06-JAN-2000; 2000WO-US000376.  
XX 11-FEB-2000; 2000WO-US003565.  
XX 18-FEB-2000; 2000WO-US004341.  
XX 18-FEB-2000; 2000WO-US004342.  
XX 02-MAR-2000; 2000WO-US005841.  
XX 03-MAR-2000; 2000US-0187202P.  
XX 10-MAR-2000; 2000WO-US006319.  
XX 15-MAR-2000; 2000WO-US006884.  
XX 30-MAR-2000; 2000WO-US008439.  
XX 17-MAY-2000; 2000WO-US013705.

(GETH ) GENENTECH INC.  
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
PI Shelton DL, Smith V, Watanabe CK, Wood WI;  
XX WPI; 2001-016509/02.  
DR N-PSDB; AAC91564.

XX Twenty eight nucleic acids encoding PRO/polypeptides which are useful for  
PT treating various tumors, e.g. breast cancer, and other inflammatory,  
PT angiogenic and immunological disorders.  
PS Claim 31; Fig 24; 188pp; English.  
XX The present sequence is one of twenty eight novel PRO polypeptides. The  
CC PRO polypeptides and their agonists, including antibodies, peptides, and  
CC small molecule agonists, may be used to treat various tumors, e.g.,  
CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal  
CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,  
CC central nervous system cancer, melanoma or leukaemia. They are also  
CC useful for treating other disorders such as neuronal, glial, astrocytal,  
CC hypothalamic and other glandular, macrophagal, epithelial, stromal and  
CC blastocoealic disorders, and inflammatory, angiogenic and immunological  
CC disorders  
XX Sequence 567 AA;

Query Match 37.0%; Score 999; DB 4; Length 567;  
Best Local Similarity 41.8%; Pred. No. 1.8e-70;  
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;  
Qy 3 LHVVKWKLVSIVLITLYSHT-VALSLKEHLADCLDKDYDTLLQTLONGLPHINTSHH 61  
Db 6 LHL-----LVLPILLSVASQDWKAERSQDPPEKCMQDPDYEQLLKVVWTWGLNRLTKPQR 61  
Qy 62 VVIVAGMAGLTAAKLQDAGHTVITILEANDRVGRVETRYNEKEGVAEMGAMRIPSSH 121  
Db 62 VVIVAGVAGLVAALKVLSAGHKVITILEADNRIGRIETFRDQNTGWIGELGAMRMPSSH 121  
Qy 122 RIVQWFKLVGWNVEFVMTDNTFVLYNGVRRTYVYVQENPDVLKYNVSESEKGISADD 181  
Db 122 RILHKLCOGLGULNTKFTQYDKNTWTEVHEVKLRNVYVEKPEKLGIALURPOEKHSPED 181  
Qy 182 LLDRALQKVEBEANGCKAALEKYDRYSVREYKKEEGSLSPGAVRMIGDILLNEQSLMYT 241  
Db 182 IYQMALNQAALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGFYFL 241  
Qy 242 ALSEMIYDQADVNSVTYHEVTGSDLLPEAFSLVDLPILLNSKVKHIRQSDKGIVISY 301  
Db 242 SFAEALRAHSCUSDRLOYSRIYGVGGWDLPRALLSSGLVLLNAPVAVMTQGHVDHVQI 301  
Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTRPD 360  
Db 302 ETSPPARNLKVLKADVLLTASGPAVKRITFSPPLPRHMQEALRLHYVPATKVFLSFR 361  
Qy 361 KFWEDDGIRGKSIITDGPRIYYPSSHFTNETIGVLLASYTWSDESLLFLGASDEELK 420  
Db 362 PFWEHEHIEGHSNTDRPSRMIFYP-----PPREGALLASYTWSDAFAAGLSREEL 416  
Qy 421 ELALRDLAKIHG---EQVMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSP- 476  
Db 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALWQTEK 466  
Qy 477 -----GRVHFAGETHAPPHAWIETSMKSIRAATNIN 508  
Db 467 DDWTPVYGRYIYFAGEHTAYPHGWVETAVKSALRAAIKIN 505

RESULT 11  
AAU12409  
ID AAU12409 standard; protein; 567 AA.

XX AAU12409;  
XX 24-OCT-2001 (first entry)  
XX Human PRO1265 polypeptide sequence.  
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;



KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping.  
OS Homo sapiens.  
PN WO200200690-A2.  
XX  
XX 03-JAN-2002.  
XX  
XX 20-JUN-2001; 2001WO-US019692.  
XX  
XX 23-JUN-2000; 2000US-02113637P.  
XX  
XX 20-JUL-2000; 2000US-0219556P.  
XX  
XX 25-JUL-2000; 2000US-0220624P.  
XX  
XX 25-JUL-2000; 2000US-0220664P.  
XX  
XX 28-JUL-2000; 2000WO-US020710.  
XX  
XX 02-AUG-2000; 2000US-0222695P.  
XX  
XX 17-AUG-2000; 2000US-00641657.  
XX  
XX 23-AUG-2000; 2000WO-US023522.  
XX  
XX 24-AUG-2000; 2000WO-US023328.  
XX  
XX 07-SEP-2000; 2000US-0230978P.  
XX  
XX 18-SEP-2000; 2000US-00664610.  
XX  
XX 18-SEP-2000; 2000US-00665350.  
XX  
XX 24-OCT-2000; 2000US-0242922P.  
XX  
XX 08-NOV-2000; 2000US-00709238.  
XX  
XX 08-NOV-2000; 2000WO-US030952.  
XX  
XX 01-NOV-2000; 2000WO-US030873.  
XX  
XX 01-DEC-2000; 2000WO-US032678.  
XX  
XX 20-DEC-2000; 2000US-00747259.  
XX  
XX 20-DEC-2000; 2000WO-US034956.  
XX  
XX 22-JAN-2001; 2001US-00767609.  
XX  
XX 28-FEB-2001; 2001US-00816744.  
XX  
XX 28-FEB-2001; 2001WO-US006520.  
XX  
XX 01-MAR-2001; 2001WO-US006666.  
XX  
XX 09-MAR-2001; 2001US-00802706.  
XX  
XX 14-MAR-2001; 2001US-00808689.  
XX  
XX 22-MAR-2001; 2001US-00816744.  
XX  
XX 05-APR-2001; 2001US-00828366.  
XX  
XX 10-MAY-2001; 2001US-00854208.  
XX  
XX 10-MAY-2001; 2001US-00854280.  
XX  
XX 25-MAY-2001; 2001US-00866028.  
XX  
XX 25-MAY-2001; 2001US-00866034.  
XX  
XX 25-MAY-2001; 2001WO-US017092.  
XX  
XX 30-MAY-2001; 2001US-00870574.  
XX  
XX 30-MAY-2001; 2001WO-US017443.  
XX  
XX 01-JUN-2001; 2001WO-US017800.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
XX WPI; 2002-090516/12.  
XX  
XX N-PSDB; ABL88159.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal.  
XX  
XX Claim 11; Fig 176; 565pp; English.  
XX  
XX ABL88072 to ABL88258 encode the PRO proteins given in ABL884817 to  
CC ABL885003. The PRO proteins and polynucleotides have cardiac, cytostatic,  
CC antiangiogenic, hypotensive, vulnary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The PRO polynucleotides have applications in molecular biology,  
CC including use as hybridisation probes, and in chromosome and gene  
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
CC exemplification of the present invention  
XX  
XX SQ Sequence 567 AA;  
XX  
XX Query Match 37.0%; Score 999; DB 5; Length 567;  
XX Best Local Similarity 41.8%; Pred. No. 1.8e-70;  
XX Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;  
QY 3 LHVVKWKLVSIVLITLYSHT-VALSLKEHLADLCEDKDYDTLQTLDNGLPHINTSHH 61  
DB 6 LHL-----LVLPVLLSLVASQDMKAERSQDPFEKCMQDPDYEQLLKVVMTGWLNRLLKPOR 61  
QY 62 VVIVGAGMAGLTAAKLLQDAGHTVILEANDRVGRVETRYNEKEGWAEKMGAMRIPSSH 121  
DB 62 VVIVGAGVAGLVAAKVLSDAGHKVILEADNRIGRITFYRDQNTGWIGELGAMRMPSSH 121  
QY 122 RIVQWFKVLGVEMNEFVMTDNTFYLVNGVRERTYVVOENPDVLKYNVSESEKISADD 181  
DB 122 RILHKLCOGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKVPKLGALRPOEKGHSPED 181  
QY 182 LLDRALQKVEVEANGCKAALEKVDYRSVREYLYKEEGLSPCAVRMIGDLLNEQSLMYT 241  
DB 182 IYQMALNQALKDLKALGCRKAMKPERHTLLEYLLGEGNLSRPAVQLLGDVMSBDGFFYL 241  
QY 242 ALSEMIYDQADVNDVTVHEVTGGDLLPEAFSLVDVPIILLNSKVKHROSQDKGVISY 301  
DB 242 SFAELRAHSCSLRLQYSRIVGGWDLPLRALLSGLVLLNAPVAVMTQPHDVHVOI 301  
QY 302 QTGNES-SLMDLSADIVLVTAKAALFIDPPPLSISKMEALRSVHYDSSTKILLTFRD 360  
DB 302 ETSPPARNLKVLRKADVLLTASGPAVKRITFSPPLPRHQEALRLHVVYPATKVFLSFPR 361  
QY 361 KFWEDDGIKGSITDGSRYIYPPSHSFHTNETIGVLLASVTSWDESLFLGASDEELK 420  
DB 362 PFWEHEIEGHGSHNTDRSRMIFYP-----PPREGALLSASYTSWDAFAAGLSREAL 416  
QY 421 ELALDLAKIHG---EQWMDCTGVIVKWSADPVLGAFALFTPYQHLEVAQELFSSE- 476  
DB 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWEDQHSQGGFVVQPP-----ALWQTEK 466  
QY 477 -----GRVHAGEHTAFPHAMTSMKSAIRAATNIN 508  
DB 467 DDWTPVPGRIYFAGEHTAYPHGWETAVKLSALRAAIKIN 505  
RESULT 13  
ABB10104  
ID ABB10104 standard; protein; 567 AA.  
XX  
XX AC ABB10104;  
XX  
XX DT 01-JUL-2002 (first entry)  
XX  
XX DE Human immediate early interleukin-four induced protein.  
XX  
XX KW Interleukin-four induced protein; IL-4; cytostatic; antifungal;  
KW antibacterial; immunomodulator; antiinflammatory; dermatological;  
KW immunosuppressive; immune disease; tumour; fungal infection;  
KW bacterial infection; systemic lupus erythematosus;  
KW inflammatory bowel disease; Guillain-Barre syndrome;  
KW atopic dermatitis; food hypersensitivity; rheumatoid arthritis;  
KW osteoarthritis; diabetes mellitus; psoriasis; gene therapy; human.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200218574-A2.  
XX  
XX PD 07-MAR-2002.  
XX  
XX PF 24-AUG-2001; 2001WO-US026462.

XX 25-AUG-2000; 2000US-0227818P.  
XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
XX Chu CC, Chavan SS, Mason JM;  
XX WPI; 2002-329772/36.  
XX New human immediate early interleukin-four (IL-4) induced protein and  
PT polynucleotides, useful for preventing or treating immune related  
PT disease, tumor, fungal or bacterial infection, e.g. lupus erythematosus  
PT or Whipple's disease.  
XX  
XX Claim 1(a); Page 5; 61pp; English.  
XX The invention relates to an isolated polynucleotide, which encodes a  
CC human immediate early interleukin-four (IL-4) induced protein. The  
CC activity of the polynucleotide of the invention may be described as,  
CC cytostatic, antifungal, antibacterial, immunomodulator, antiinflammatory,  
CC dermatologic and immunosuppressive. The polynucleotide or antisense  
CC oligonucleotide is useful for the manufacture of a medicament for  
CC preventing, treating or ameliorating a medical condition, particularly  
CC immune related disease, tumour, fungal infection or bacterial infection.  
CC The immediate early IL-4 induced protein is useful for the manufacture of  
CC a medicament for killing unwanted cells in a mammal. The antagonist is  
CC useful for the manufacture of a medicament for use in decreasing cell  
CC death. The polynucleotide is also useful for diagnosing a pathological  
CC condition, particularly an immune related disease. These diseases may  
CC include systemic lupus erythematosus, inflammatory bowel disease,  
CC Guillain-Barre syndrome, Whipple's disease, atopic dermatitis, food  
CC hypersensitivity, rheumatoid arthritis, osteoarthritis, diabetes mellitus  
CC and psoriasis. The polynucleotide of the invention may be used in gene  
CC therapy. The current sequence represents a human immediate early  
CC interleukin-four induced protein. Note: This sequence should be encoded  
CC by the DNA sequence given in the specification as SEQ ID 3 (Human  
CC immediate early interleukin-four induced protein genomic DNA from  
CC chromosome 19q13.3-19q13.4 - see ABL56822), however, this does not appear  
XX to be the case  
XX  
XX Sequence 567 AA;  
Query Match 37.0%; Score 999; DB 5; Length 567;  
Best Local Similarity 41.8%; Pred. No. 1.8e-70;  
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;  
3 LHVVKWKLVSVLITLYSHT-VALSLKEHLADCLDKDYTLTLQNLGPHLNTSHH 61  
6 LHL-----LVLVPIILLSVASODWKAERSQDPPEKCMQDPDYEQLLKVVWGLNRLTKPQR 61  
62 VVIVGAGMAGLTAALKLODAGHTVTILEANDRVGGRVETVNEKEGWAEMGAMRTPSSH 121  
62 VIVVGAGVAGLVAALKVLSADGAKVTTLEADNRIGGRIFTRDQNTGIGELGAMRWPSH 121  
122 RIYQWFKVLGVENNEFVMTDDNTFYLVNGVRRVTYVQENPDVLKYNVSESEKGISAD 181  
122 RILHLKCGGLNLTKFTQDKNTWTEVHEVKLRNVYVKEKLGVALRPOKGHSPED 181  
182 LLDRALQKVEEANGKAALEKYDRYSVKVEYKKEGGSLPGAVRMIGDLLNEQSLMYT 241  
182 IYQMALNQALKDKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDEGFFYL 241  
242 ALSEMIYDQADVNDVTVYHETGSGDLLPEAFSLVDLPVILLNSKVKHQRQSDKGVIVSY 301  
242 SFAELRAHSCLSRLQVSRIVGWDLLPRALLSGLVLLNAPVVMVMTQGHDPVHVQI 301  
302 QTGNES-SLMDLSADIVLVTTAKAALFIDFPPLSLISKWEALRSVHYDSSTKILITFRD 360  
302 ETSPPARNLKVLDKADVLLTAGSPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFR 361  
361 KFWEDDGIKGSKSTDGPSRVIYYPSPSHFNTETIGVLLASYTWSDESLLPLGASDBELK 420  
362 PFWRREEHIEGGHNSNDRPSRMIFYP-----PPREGALLLASYTWSDAAFAGLSREAL 416

QY 421 ELALRDLAKIHG---EQVWDKCTGVIVKWSADPYSGLGAFALFTPYQHLVYAQELFSSE- 476  
DB RLALDDVAALHGFVVRQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALMQTEK 466  
QY 477 -----GRVHEFAGEHTAPPHAWIETSMKSAIRAATNIN 508  
DB DDWTVPYGRYIYFAGEHTAYPHGCVETAVKSALRAAKIN 505  
RESULT 14  
ABB95510  
ID ABB95510 standard; protein; 567 AA.  
XX ABB95510;  
XX 19-JUL-2002 (first entry)  
XX Human angiogenesis related protein PRO1265 SEQ ID NO: 176.  
DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;  
KW antiarteriosclerotic.  
XX Homo sapiens.  
OS WO200208284-A2.  
XX 31-JAN-2002.  
XX 09-JUL-2001; 2001WO-US021735.  
XX 20-JUL-2000; 2000US-0219556P.  
XX 25-JUL-2000; 2000US-0220624P.  
XX 25-JUL-2000; 2000US-0220664P.  
XX 28-JUL-2000; 2000WO-US020710.  
XX 02-AUG-2000; 2000US-0222695P.  
XX 17-AUG-2000; 2000US-00643657.  
XX 23-AUG-2000; 2000WO-US023522.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 07-SEP-2000; 2000US-0230978P.  
XX 18-SEP-2000; 2000US-00664610.  
XX 18-SEP-2000; 2000US-00665350.  
XX 24-OCT-2000; 2000US-0242922P.  
XX 08-NOV-2000; 2000US-00709238.  
XX 08-NOV-2000; 2000WO-US030952.  
XX 10-NOV-2000; 2000WO-US030873.  
XX 01-DEC-2000; 2000WO-US032578.  
XX 20-DEC-2000; 2000US-00747259.  
XX 22-DEC-2000; 2000WO-US034956.  
XX 28-FEB-2001; 2001US-00767609.  
XX 28-FEB-2001; 2001US-00796498.  
XX 01-MAR-2001; 2001WO-US006520.  
XX 09-MAR-2001; 2001US-00802706.  
XX 14-MAR-2001; 2001US-00808689.  
XX 22-MAR-2001; 2001US-00816744.  
XX 05-APR-2001; 2001US-00828366.  
XX 10-MAY-2001; 2001US-00854208.  
XX 10-MAY-2001; 2001US-00854280.  
XX 25-MAY-2001; 2001US-00866028.  
XX 25-MAY-2001; 2001US-00866034.  
XX 25-MAY-2001; 2001WO-US017092.  
XX 30-MAY-2001; 2001US-00870574.  
XX 30-MAY-2001; 2001WO-US017443.  
XX 01-JUN-2001; 2001WO-US017800.  
XX 20-JUN-2001; 2001WO-US019692.  
XX (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.



```

PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015284.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001US-00065520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001US-00920116.
PR 29-JUN-2001; 2001WO-US021060.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Geritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX WPI; 2003-341980/32.
XX N-PSDB; ACD24090.
XX New secreted and transmembrane PRO nucleic acids, for treating
XX inflammation, organ failure, atherosclerosis, cardiac injury,
XX infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX Claim 12; Fig 476; 660pp; English.
XX The invention describes an isolated nucleic acid (I) comprising, or which
XX has 80 % sequence identity to, or the full-length coding sequence of, one
XX of 275 nucleotide sequences, and which encodes a corresponding
XX polypeptide selected from 275 amino acid sequences, where all sequences
XX are given in the specification. The polypeptide encoded by (I) is used to
XX detect PRO polypeptides, link a bioactive molecule to a cell expressing a
XX PRO polypeptide, modulate a biological activity of a cell, stimulate the
XX release of tumour necrosis factor (TNF)-alpha from human blood, modulate
XX the uptake of glucose or free fatty acid by cells, stimulate or inhibit
XX the proliferation or differentiation of cells or gene expression,
XX stimulate the release of proteoglycans, stimulate the release of cytokine
XX from peripheral blood mononuclear cells, inhibit the binding of A-peptide
XX to factor VIIa, or detect the presence of tumour in a mammal. The nucleic
XX acid and polypeptide encoded by it, are useful for treating inflammatory
XX diseases, organ failure, atherosclerosis, cardiac injury, infertility,
XX birth defects, premature aging, acquired immunodeficiency syndrome
XX (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
XX hybridisation probes, in chromosome and gene mapping, and in generating
XX antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
XX diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
XX This is the amino acid sequence of a novel human secreted and
XX transmembrane PRO polypeptide
XX Sequence 567 AA;
SQ
Query Match 37.0%; Score 999; DB 6; Length 567;
Best Local Similarity 41.8%; Pred. No. 1.8e-70;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;
QY 3 LHVVKWKLVSVLTLYYSHT-VALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSHH 61
DB 6 LHL-----LVLVPIILLSVASQDWKAERSQDPFEKMQDPDYQLKVVYWGNTLTKFQR 61
QY 62 VVIVGAGMAGLTAAKLQDAGHTVTILEANDRVGRVETRYRNEKEXGYAEMGAMRIPSSH 121
DB 62 VIVVGAGVAGLVAALKVSLDAGHKVTILEADNRIGRIFTYRDQNTGIGELGAMRMPSSH 121
QY 122 RIVQVFKVLGVENEFWTDNDTFFYLVNGVRITYVVOENPDVLKYNVSEKGISADD 181
DB 122 RILHKLQGLNLTKFTQYDKNTWTEVHEKLRNVYVKEVPEKLGVALRPOEKHSPED 181
QY 182 LLDRALOKVKEEANGCKAALEKDYRVSVKYLKEEGLSPGAVRMIGDLLNEOSLMYT 241
DB 182 IYQNALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLRPAVOLLCGVSEDFYFL 241
QY 242 ALSEMIYDQADVNDVTVYHEVTGGSDLLPEAFSLVDLPVILLNSKVGHROSDKGVIVSY 301
DB 242 SFAEALRAHSCLSRLQVSRIVGCGWDLPLRALLSSLSGLVLLNAPVAVMTQPHDVHVI 301
QY 302 QTGNES-SLMDLSADIVLVTAKAALFIDPDPPLISKMEALRSVHYDSSTKILLTRD 360
DB 302 ETSPPARNLKVLLKADVLLLTASGPAVKRITFSPPLPRHMQALRLRLHVVPAKVFLSRR 361
QY 361 KFWEDDGIKGGKSIITDGPRIYVYPSHSFHTNETIGVLLASVTSWSEILLFLGASDEELK 420
DB 362 PFWEHEHIEGHSNTDRSRMIFYP-----PPREGALLLASYTWSDDAAAFAGLSREAL 416
QY 421 ELALRDLAKIHG---EQWMDKCTGIVVKWSADPYSLGAFALFTPYQHLEVAQELFSSE- 476
DB 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGVVQPP-----ALWQTEK 466
QY 477 -----GRVHFAGEHTAPPHAWTETSMSKSAIRAATNIN 508
DB 467 DDWTPVYGRYIFAGEHTAYPHGWTETAVKSALRAAIKIN 505

```

Search completed: October 4, 2005, 14:03:38

Job time : 170 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 13:32:30 ; Search time 43 Seconds  
(without alignments)  
909.677 Million cell updates/sec

Title: US-10-645-094-1  
Perfect score: 2703  
Sequence: 1 MNLHVVKWKLVSVLITLY.....TNINKVANEESTIHTKDEL 524

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2703	100.0	524	US-09-230-388-1	Sequence 1, Appli
2	2703	100.0	524	US-09-912-176-1	Sequence 1, Appli
3	999	37.0	567	US-08-813-150-4	Sequence 4, Appli
4	999	37.0	567	US-09-546-553-4	Sequence 4, Appli
5	979.5	36.2	566	US-09-482-273-173	Sequence 173, App
6	488.5	18.1	319	US-09-482-273-267	Sequence 267, App
7	488.5	18.1	320	US-09-482-273-194	Sequence 194, App
8	476	17.6	275	US-09-482-273-265	Sequence 265, App
9	417	15.4	617	US-09-063-733A-46	Sequence 46, Appl
10	417	15.4	617	US-09-063-733A-56	Sequence 56, Appl
11	417	15.4	617	US-09-063-733A-57	Sequence 57, Appl
12	417	15.4	617	US-09-063-733A-58	Sequence 58, Appl
13	404	14.9	617	US-09-314-242-2	Sequence 2, Appli
14	392	14.5	695	US-09-314-242-12	Sequence 12, Appl
15	387	14.3	212	US-09-482-273-266	Sequence 266, App
16	364.5	13.5	489	US-09-986-536-2	Sequence 2, Appli
17	307	11.4	538	US-09-252-991A-16952	Sequence 16952, A
18	294	10.9	545	US-09-949-016-11442	Sequence 11442, A
19	283	10.5	527	US-08-132-168A-32	Sequence 32, Appl
20	283	10.5	531	US-09-949-016-11443	Sequence 11443, A
21	258	9.5	733	US-09-073-587-3	Sequence 3, Appli
22	211.5	7.8	458	US-09-328-352-7549	Sequence 7549, Ap
23	197.5	7.3	554	US-09-352-159-17	Sequence 17, Appl
24	197.5	7.3	554	US-09-352-168-17	Sequence 17, Appl
25	197.5	7.3	554	US-09-771-045B-17	Sequence 17, Appl
26	197.5	7.3	554	US-09-770-564A-17	Sequence 17, Appl
27	196.5	7.3	463	US-09-771-045B-51	Sequence 51, Appl

28	195.5	7.2	463	4	US-09-771-045B-53	Sequence 53, Appl
29	195	7.2	487	3	US-09-352-159-21	Sequence 21, Appl
30	195	7.2	487	3	US-09-352-168-21	Sequence 21, Appl
31	195	7.2	487	4	US-09-771-045B-21	Sequence 21, Appl
32	195	7.2	487	4	US-09-770-564A-21	Sequence 21, Appl
33	194.5	7.2	463	4	US-09-771-045B-49	Sequence 49, Appl
34	193.5	7.2	600	3	US-09-352-159-36	Sequence 36, Appl
35	193.5	7.2	600	3	US-09-352-159-38	Sequence 38, Appl
36	193.5	7.2	600	4	US-09-771-045B-36	Sequence 36, Appl
37	193.5	7.2	600	4	US-09-771-045B-38	Sequence 38, Appl
38	193.5	7.2	600	4	US-09-882-694B-23	Sequence 23, Appl
39	193.5	7.2	600	4	US-09-882-694B-25	Sequence 25, Appl
40	192.5	7.1	600	4	US-09-771-045B-33	Sequence 33, Appl
41	192.5	7.1	829	3	US-09-352-159-33	Sequence 33, Appl
42	192.5	7.1	829	3	US-09-352-168-33	Sequence 33, Appl
43	192.5	7.1	829	4	US-09-770-564A-33	Sequence 33, Appl
44	191.5	7.1	462	3	US-09-352-159-6	Sequence 6, Appli
45	191.5	7.1	462	3	US-09-352-159-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-09-230-388-1  
; Sequence 1, Application US/09230388  
; Patent No. 6291644  
; GENERAL INFORMATION:  
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-kee  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING  
; FILE REFERENCE: 4703/OF214  
; CURRENT APPLICATION NUMBER: US/09/230,388  
; PRIOR FILING DATE: 1999-01-23  
; PRIOR APPLICATION NUMBER: PCT/JP98/02261  
; PRIOR FILING DATE: 1998-05-22  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 524  
; TYPE: PRT  
; ORGANISM: Scomber japonicus  
US-09-230-388-1

Query Match	100.0%;	Score	2703;	DB 3;	Length	524;	
Best Local Similarity	100.0%;	Pred. No.	3.6e-239;	Mismatches	0;	Gaps	0;
Matches	524;	Conservative	0;	Indels	0;		
Qy	1	MNLHVVKWKLVS	VSLITLYSHTVALSKKHLADCLDKDYDTLLQTLNDNLGLPHINTSH	60			
Db	1	MNLHVVKWKLVS	VSLITLYSHTVALSKKHLADCLDKDYDTLLQTLNDNLGLPHINTSH	60			
Qy	61	HVIVGAGMAGLTA	AKLLQDAGHTVTILEANDRVGGRVETVYRNEKEGWAEMGARIPSS	120			
Db	61	HVIVGAGMAGLTA	AKLLQDAGHTVTILEANDRVGGRVETVYRNEKEGWAEMGARIPSS	120			
Qy	121	HRIVQVFKVLGYEMNEFVMTDDNTFYLNGVRERTYVQENPDVLYKNVSESEKGISAD	180				
Db	121	HRIVQVFKVLGYEMNEFVMTDDNTFYLNGVRERTYVQENPDVLYKNVSESEKGISAD	180				
Qy	181	DLDRALQVKKEEVEANGCKAALEKYDRYSVKYELKEEGGLSPGAVRMIGDLLNEQSLMY	240				
Db	181	DLDRALQVKKEEVEANGCKAALEKYDRYSVKYELKEEGGLSPGAVRMIGDLLNEQSLMY	240				
Qy	241	TALSEMIYDQADVNDSVTYHEVTGSGDLLPEAFVLSLDVPILLNSKVKHIRQSKGVIVS	300				
Db	241	TALSEMIYDQADVNDSVTYHEVTGSGDLLPEAFVLSLDVPILLNSKVKHIRQSKGVIVS	300				
Qy	301	YQTCNESSLMDLSADIVLVTTTAKAALFIQDPPLSISKMEALRSVHYDSSTKILLTFRD	360				
Db	301	YQTCNESSLMDLSADIVLVTTTAKAALFIQDPPLSISKMEALRSVHYDSSTKILLTFRD	360				
Qy	361	KFWEDDGIRGKGSITDGPSSRYIYYPSHSPHFTNETIGVLLASYTWSDESLLFLGASDEELK	420				

```
Db 361 KFWDDGIRGKSIITDPSRIYYPSHFHNETIGVLLASYTWSDESLFLGASDEELK 420
QY 421 ELALRDLAKIHGEQWMDKCTGVIVKWSADPYSGLGAPALFTPYQHLEYVAQELFSSEGRVH 480
Db 421 ELALRDLAKIHGEQWMDKCTGVIVKWSADPYSGLGAPALFTPYQHLEYVAQELFSSEGRVH 480
QY 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIETHTKDEL 524
Db 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIETHTKDEL 524

RESULT 2
US-09-912-176-1
; Sequence 1, Application US/09912176
; Patent No. 6649739
; GENERAL INFORMATION:
; APPLICANT: Iwamoto, Mitsunori, Jung, Sang-kee
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING
; TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS
; FILE REFERENCE: 4703/0F214
; CURRENT APPLICATION NUMBER: US/09/912,176
; PRIOR FILING DATE: 2001-07-24
; PRIOR FILING DATE: 2001/07/24
; PRIOR APPLICATION NUMBER: US 09/230,388
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: PCT/JP98/02261
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Scomber japonicus
US-09-912-176-1

Query Match 100.0%; Score 2703; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 3.6e-239;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNLHVVKWLSVSVLITLYSHTVALSLKEHLADCLEDKDYDTLLQTLNGLPHINTSH 60
Db 1 MNLHVVKWLSVSVLITLYSHTVALSLKEHLADCLEDKDYDTLLQTLNGLPHINTSH 60
QY 61 HVVIVGAGWAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGVAEMGAMRIPSS 120
Db 61 HVVIVGAGWAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGVAEMGAMRIPSS 120
QY 121 HRIVQFVKVLGVEMNEFVMTDDNTFYLVNGVRERTYVVOENPDVLYKNVSESEKISAD 180
Db 121 HRIVQFVKVLGVEMNEFVMTDDNTFYLVNGVRERTYVVOENPDVLYKNVSESEKISAD 180
QY 181 DLLDRALQKVKEVEANGCKAALKYDYSVKEYLKEEGGLSPGAVRMIGDILLNEQSLMY 240
Db 181 DLLDRALQKVKEVEANGCKAALKYDYSVKEYLKEEGGLSPGAVRMIGDILLNEQSLMY 240
QY 241 TALSEMIYQDADVNDVSVTYHEVTGSDLLPEAFSLVDVPILLNSKVHROSQKGVIVS 300
Db 241 TALSEMIYQDADVNDVSVTYHEVTGSDLLPEAFSLVDVPILLNSKVHROSQKGVIVS 300
QY 301 YQTGNESLMDLSADIVLVTAKAALFIDFPPLSISKWEALRSVHYDSSTKILLTFRD 360
Db 301 YQTGNESLMDLSADIVLVTAKAALFIDFPPLSISKWEALRSVHYDSSTKILLTFRD 360
QY 361 KFWDDGIRGKSIITDPSRIYYPSHFHNETIGVLLASYTWSDESLFLGASDEELK 420
Db 361 KFWDDGIRGKSIITDPSRIYYPSHFHNETIGVLLASYTWSDESLFLGASDEELK 420
QY 421 ELALRDLAKIHGEQWMDKCTGVIVKWSADPYSGLGAPALFTPYQHLEYVAQELFSSEGRVH 480
Db 421 ELALRDLAKIHGEQWMDKCTGVIVKWSADPYSGLGAPALFTPYQHLEYVAQELFSSEGRVH 480
QY 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIETHTKDEL 524
```

```
Db 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIETHTKDEL 524

RESULT 3
US-08-813-150-4
; Sequence 4, Application US/08813150
; Patent No. 6069229
; GENERAL INFORMATION:
; APPLICANT: Mueller, Christopher
; APPLICANT: Lebecque, Serge J.E.
; APPLICANT: Liu, Yong-Jun
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Huffine, Constance M.
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN PROTEINASES; OXIDOREDUCTASES;
; NUMBER OF SEQUENCES: 6
; TITLE OF INVENTION: RELATED REAGENTS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/813,150
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SP0693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 567 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-813-150-4

Query Match 37.0%; Score 999; DB 3; Length 567;
Best Local Similarity 41.8%; Pred. No. 9.3e-83;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVVKWLSVSVLITLYSHT-VALSLKEHLADCLEDKDYDTLLQTLNGLPHINTSHH 61
Db 6 LHL-----LVLVPIILLSVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTVGLNLTLPQR 61
QY 62 VVIVGAGWAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGVAEMGAMRIPSSH 121
Db 62 VVIVGAGWAGLVAARVSDAGHKVTILEADNRIGRTTYRDQNTGWIGELGAMRMPSSH 121
QY 122 RIVQFVKVLGVEMNEFVMTDDNTFYLVNGVRERTYVVOENPDVLYKNVSESEKISADD 181
Db 122 RILHLKLCQGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKVPKGLVALRPOEKHSPED 181
QY 182 LLDRALQKVKEVEANGCKAALKYDYSVKEYLKEEGGLSPGAVRMIGDILLNEQSLMYT 241
Db 182 IYQMALNQALDKALGCRKAMKPFERTLTLEYLLLEGNLSPAVQLLGDVMSDEGFFYL 241
QY 242 ALSEMIYQDADVNDVSVTYHEVTGSDLLPEAFSLVDVPILLNSKVHROSQKGVIVSY 301
Db 242 SFAEALRAHSCLSRLQYSRIVGVGWDLLPRALLSSLSGLVLLNAPVAVMTQCPHDVHVI 301
```



Db 122 RILHLKCOGLGNTLTKFTQYDKNTWTEVHEVKLRNVVVEKPEKLGVALRPOEKHSPED 181  
Qy 182 LLDRLALQKVEEANGCKAALKEKYDRYSVKYELKEEGSLSPGAVRMTGDLNLSQSLMYT 241  
Db 182 IYQMALNQALKDLKALGCRKAMKPERHTLLEYLLEGNLSRPAVQLLGDVMSDEGFFYL 241  
Qy 242 ALSEMIYDQADVNDSTVTHEVTGSDLLPEAFSLVDLPILNSKVKHQRSKGVIVSY 301  
Db 242 SFAEALRAHSCUSDRLOYSRIVGGWDLPRALLSSLSGLVLLNAPVAVMTQGGPHDVHVOI 301  
Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFDPPLSISKMAELRSVHYDSSTKILLTPRD 360  
Db 302 ETSPPARNLKVADVLLTAGSPAVKRTSPPLPRHQEALRHLHYVPATKVLFSRPR 361  
Qy 361 KFEWDDGIRGKSIITDGPRIYIYPSHFHTNETTGVLLASVTWSDESLLFLGASDEBLK 420  
Db 362 PFWREHEIGHSHNTDRPSRMIFYP-----PPREGALLASVTWSDAFAAGLSREBAL 416  
Qy 421 ELALRDLAKIHG---EQWWDKCTGVIVKWSADPYSLSGAFALFTPYQHLEYAQELFSSE- 476  
Db 417 RLALDDVAALHGFVVRQLWDG-TGV-VKRWAEQHSQGGFVVOPP-----ALWQTEK 466  
Qy 477 -----GRVHPAGEHTAPPHAWIETSMKSALRAATNIN 508  
Db 467 DDMVTVPYGRIFYAGEHTAYPHGAVETAVK-LLRAAIKIN 504

RESULT 6  
US-09-482-273-267  
; Sequence 267, Application US/09482273  
; Patent No. 6534631  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 71 Human Secreted Proteins  
; FILE REFERENCE: P2030P1  
; CURRENT APPLICATION NUMBER: US/09/482,273  
; CURRENT FILING DATE: 2000-01-13  
; EARLIER APPLICATION NUMBER: PCT/US99/15849  
; EARLIER FILING DATE: 1999-07-14  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,922  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,956  
; EARLIER FILING DATE: 1998-07-15  
; NUMBER OF SEQ ID NOS: 267  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 267  
; LENGTH: 319  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (68)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (115)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (213)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (320)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-482-273-267

Query Match 19.1%; Score 488.5; DB 4; Length 319;  
Best Local Similarity 33.6%; Pred. No. 2.5e-36;  
Matches 112; Conservative 69; Mismatches 109; Indels 43; Gaps 4;  
Qy 3 LHVVKWKLSSVSVLITLYSHT-VALSLKEHLADCLDEKDYDTLLQTLNDGLPHINTSHH 61  
Db 6 LHL-----LVLVPIILLSVASQDWKERSQDPFEKCMQDPDYQLLK----- 47

Qy 62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRVGGRVETVYRNEKEGVAEMGAMRIPSSH 121  
Db 48 -----VTILEADNRIGGRIFTYRDQXTGWIIGELGAMRPSSH 84  
Qy 122 RIYQWFKVLGVEMNEFVMTDDNTFYLVNGVRERTTVVQENPDVLKYNVSESEKGI SADD 181  
Db 85 RILHLKCOGLGNTLTKFTQYDKNTWTEVHEVKLRNVVVEKPEKLGVALRPOEKHSPED 144  
Qy 182 LLDRLALQKVEEANGCKAALKEKYDRYSVKYELKEEGSLSPGAVRMTGDLNLSQSLMYT 241  
Db 145 IYQMALNQALKDLKALGCRKAMKPERHTLLEYLLEGNLSRPAVQLLGDVMSDEGFFYL 204  
Qy 242 ALSEMIYDQADVNDSTVTHEVTGSDLLPEAFSLVDLPILNSKVKHQRSKGVIVSY 301  
Db 205 SFAEALRAHSCUSDRLOYSRIVGGWDLPRALLSSLSGLVLLNAPVAVMTQGGPHDVHVOI 264  
Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFDP 333  
Db 265 ETSPPARNLKVADVLLTAGSPAVKRTITSP 297

RESULT 7  
US-09-482-273-194  
; Sequence 194, Application US/09482273  
; Patent No. 6534631  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 71 Human Secreted Proteins  
; FILE REFERENCE: P2030P1  
; CURRENT APPLICATION NUMBER: US/09/482,273  
; CURRENT FILING DATE: 2000-01-13  
; EARLIER APPLICATION NUMBER: PCT/US99/15849  
; EARLIER FILING DATE: 1999-07-14  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,922  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,956  
; EARLIER FILING DATE: 1998-07-15  
; NUMBER OF SEQ ID NOS: 267  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 194  
; LENGTH: 320  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (68)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (115)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (213)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (320)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-482-273-194

Query Match 18.1%; Score 488.5; DB 4; Length 320;  
Best Local Similarity 33.6%; Pred. No. 2.6e-36;  
Matches 112; Conservative 69; Mismatches 109; Indels 43; Gaps 4;  
Qy 3 LHVVKWKLSSVSVLITLYSHT-VALSLKEHLADCLDEKDYDTLLQTLNDGLPHINTSHH 61  
Db 6 LHL-----LVLVPIILLSVASQDWKERSQDPFEKCMQDPDYQLLK----- 47  
Qy 62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRVGGRVETVYRNEKEGVAEMGAMRIPSSH 121

Db 48 -----VTILEADNRIGGRIFTYRDOXTGWIIGELGAMRPPSH 84  
Qy 122 RIVQWFKKLGVMNEFVMTDNTFVLVNGVRERTYVVOENPDVLKYNVSESEKGISADD 181  
Db 85 RILHKLCOGLGLNLTKFTQYDKNTWTEVHEXKLRLNVVVEKPEKGLGYALRPOEGHSPED 144  
Qy 182 LLDLALOKYKEEVEANGCAALEKYDRYSVKYLBEEGGLSGAVRMIGDLNLEOSLMYT 241  
Db 145 IYQMALNQALKOLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVOLLDGVMSEDDGFFYL 204  
Qy 242 ALSEMIYDOADVNDVSYVYHEVTGSGDLPALPEAFSLVDVPILLNSKVYKHRSQDKGVINSY 301  
Db 205 SPAEALRAXSCLSDRQYRIYVGGMDLPRALLSSLSGLVLLNAPVAMTQPHDVHQI 264  
Qy 302 QTGNES-SLMDLSADIVLVTTAKAALFIDFDP 333  
Db 265 ETSPARNLKVLDKADVLLTASGPAVKRITFSP 297

RESULT 8

US-09-482-273-265  
; Sequence 265, Application US/09482273  
; Patent No. 6534631  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 71 Human Secreted Proteins  
; FILE REFERENCE: P2030P1  
; CURRENT APPLICATION NUMBER: US/09/482,273  
; EARLIER APPLICATION NUMBER: PCT/US99/15849  
; EARLIER FILING DATE: 2000-01-13  
; EARLIER FILING DATE: 1999-07-14  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER FILING DATE: 1998-07-15  
; NUMBER OF SEQ ID NOS: 267  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 265  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (47)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (94)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (192)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-482-273-265

Query Match 17.6%; Score 476; DB 4; Length 275;  
Best Local Similarity 34.7%; Pred. No. 2.8e-35;  
Matches 103; Conservative 62; Mismatches 94; Indels 38; Gaps 2;  
Qy 36 CLEDKDYDTLLQTLONGPLHINTSHHVIVGAGMAGLTAALKLQDAGHTVTILEANDRVG 95  
Db 15 CMQDPDYEQLK-----VTILEADNRIG 37  
Qy 96 GRVETRYNEKEGWAEAMGAMRIPSSHRIVQWFKKLGVMNEFVMTDNTFVLNNGVRER 155  
Db 38 GRIFTYRQXTGWIGELGAMRPPSHRILHKLCOGLGLNLTKFTQYDKNTWTEVHEXKLR 97  
Qy 156 TVVQVENPDVLKYNVSESEKGISADDLDRALOKYKEEVEANGCAALEKYDRYSVKYL 215  
Db 98 NYVVEKPEKGLYALRPOEGHSPEDIYQMALNQALKOLKALGCRKAMKKFERHTLLEYL 157

Qy 216 KBEGLSPCAVRMIGDLNLEQSLMYTALSEMIYDOADVNDVSYVYHEVTGSGDLPALPEAFUS 275  
Db 158 LLEGNLSRPAVOLLDGVMSEDDGFFYLSFAEALRAXSCLSDRQYSRIVGGMWLLPRALLS 217  
Qy 276 VLDVPIILLNSKVYKHRSQDKGVINSYQTGNES-SLMDLSADIVLVTTAKAALFIDF 331  
Db 218 SLSGLVLLNAPVAMTQPHDVHQIETSPARNLKVLDKADVLLTASGPAVKRITF 274

RESULT 9

US-09-063-733A-46  
; Sequence 46, Application US/09063733A  
; Patent No. 6372211  
; GENERAL INFORMATION:  
; APPLICANT: Isaac, Barbara G.  
; APPLICANT: Greenplate, John T.  
; APPLICANT: Purcell, John P.  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold White & Durkee  
; STREET: PO Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/063,733A  
; FILING DATE: 21-APR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT:022  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713-787-1400  
; TELEFAX: 713-787-1440  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 617 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
US-09-063-733A-46

Query Match 15.4%; Score 417; DB 3; Length 617;  
Best Local Similarity 31.0%; Pred. No. 2.7e-29;  
Matches 156; Conservative 83; Mismatches 177; Indels 88; Gaps 26;  
Qy 62 VVIWAGMAGLTAALKLQD---AGHTVTILEANDRVGGRVET--YRNEKEGWAEAMGAMR 116  
Db 87 VCIWAGVSGLIYAMILDDDLKIPNLTYDIFESSRTGRLYTHHTFDKADHYI-DIGAMR 145  
Qy 117 ---IPSSHRIVQWFKKLGVMNEFVMTDNTFVLN-----GYRERTYVYVQENPDVLK 167  
Db 146 YPDIPSMKRTNLF-KRTGMPLIKYLDGENTPOLYNNHFFAKGVD-----P 192  
Qy 168 YNVSESEKGISADDLDRALOKV-----KEEVEANGCA--ALEKYDRYSVKYLBKE 218  
Db 193 YMWVANGGTVPDDVVDVSGEKLOQAFGYKKEKLAEDPKGDFDELMVLVDDMTTREYLKRG 252  
Qy 219 G--GLSPG----AVRMIGDLNLEOSLMYALSEMIYDOADVNDV--TYHEVTGSGDLP 270  
Db 253 GPKGEAPKYDFPAIOWMETQNTGTNLFDOAFSEVSDSFDNPTKPEWYCIEGTSLLV 312  
Qy 271 EAFSLVDVPILLNSKVKHIR----QSKDGIVSYQTGNESSLMDLSADIVLVTTAKAA 326

Db	313	DAMKETLVHKVQNNKRVDAISIDLDPDGG-NMSVRIGGK-----DHSGYSTVFNTTALGC	367
Qy	327	L-----FIDFPPPLSISKMEALRSVHYDSSTKILLTFRDKFW-EDDGIR-GGKSITDGP	378
Db	368	LORDMLRGLNLHP-----TQADAIRCLHYDNSTKVALKFSYPWWIKDCGITCGGGAASDLP	423
Qy	379	SRIVYYPBSHF-HTNETIGVLLASVTWDSLSLLFLGA-----SDEELKELALRDL	427
Db	424	LRTCVPSYNLDDTGE--AVLLASTYWSQDATR-IGSLVKDAPQPQPKEDLVELLQNL	480
Qy	428	AKIHG-----EQWMDKCTGVI-VKKWSADPYSLGAFALFTPYQHLEVAQELF--SSGRV	479
Db	481	ARLHAEMTYEKIKEYATGVVHAYCWANDPNVGGAFALFGPQFSNLYPYLMRPAAGGKF	540
Qy	480	HPAGEHTAPPHAWIETSMKSASIRA 503	
Db	541	HIVGEASSVHHAWIIGSLESAYTA 564	
RESULT 10			
US-09-063-733A-56			
; Sequence 56, Application US/09063733A			
; Patent No. 6372211			
; GENERAL INFORMATION:			
; APPLICANT: Isaac, Barbara G.			
; APPLICANT: Greenplate, John T.			
; APPLICANT: Purcell, John P.			
; APPLICANT: Romano, Charles P.			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING			
; TITLE OF INVENTION: INSECTS			
; NUMBER OF SEQUENCES: 58			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Arnold White & Durkee			
; STREET: PO Box 4433			
; CITY: Houston			
; STATE: TX			
; COUNTRY: USA			
; ZIP: 77210-4433			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/063,733A			
; FILING DATE: 21-APR-1998			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Patterson, Melinda L.			
; REGISTRATION NUMBER: 33,062			
; REFERENCE/DOCKET NUMBER: MOBT:022			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 713-787-1400			
; TELEFAX: 713-787-1440			
; INFORMATION FOR SEQ ID NO: 56:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 617 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: not relevant			
; TOPOLOGY: linear			
US-09-063-733A-56			
Query Match 15.4%; Score 417; DB 3; Length 617;			
Best Local Similarity 31.0%; Pred. No. 2.7e-29;			
Matches 156; Conservative			
Qy	62	VVIYGAGMAGLTAARLQD---AGHTVTILEANDRVGRVET--YRNEKEGVAENGAMR	116
Db	87	VCIVGAGVSGLYIAMILLDLKIPNLTYDIFESSRGTGRLYTHFTDAKHYY-DIGAMR	145
Qy	117	---TPSSHRIYQWFKVLGVEMFEVMTDNTFTLVN-----GVERTYVYQENPDVLK	167

```
Query Match 15.4%; Score 417; DB 3; Length 617;
Best Local Similarity 31.0%; Pred. No. 2.7e-29;
Matches 156; Conservative 83; Mismatches 177; Indels 88; Gaps 26;

QY 62 VVIVGAGMAGLTAALKLQD---AGHTVTILEANDRVGGRVET--YRNEKEGHYAENGAMR 116
DB 87 VCIVGAGVSGLYIAMILDDLKIPNLTYDIFESSRTGGRLYTHHFTDAKHYY-DIGAMR 145
QY 117 ---IPSSHRIVQWFKVLGVEMNEFVMTDDNTFYLVN-----GVRERTYVVQENPDVLK 167
DB 146 YPDIPSMKRTNLP-KRTGMPLIKYLLDGENTPQLYNNHFFAKGVSD-----P 192
QY 168 YNVSESEKISADLLDRALQV-----KEEVEANGCKA--ALEKYDRYSVKYELKBE 218
DB 193 YMVSVANGGTVPDDVVDVSVGEKLQQAFCGYKELAEFDKGFDELMLVDDMTTREVLYKRG 252
QY 219 G--GLSPG---AVRMIGDLLNEQSLMYTALSEMIYDQADVNSV--TYHEVTGSGDLLP 270
DB 253 GPKGEAPKYDFFAIQMMETQNTGTNLFDQAFSEVIDSFDFONPTKPEWYCIEGGTSLLV 312
QY 271 EAFSLVDVPIILLNSKVKHIR----QSDKGIVSVYOTGNESLMDLSADIVLVTITAKAA 326
DB 313 DAMKETLVHKVQNNKRVDAISIDLDPDGG-NMSVRIGGK----DHSGYSTVNTTALGC 367
QY 327 L-----FIDFPPPLISKMEALRSVHYDSSTKILLTFRDKFW-BDDGIR-GGKSITDGP 378
DB 368 LDRMDLRLGLNLHP---TQADAIRCLHYDNSTKVALKFSYPWMIKDCGTCGGAASDLP 423
QY 379 SRYIYYPSSHSP-HTNETIGVLLASTYWSDESLLFLGA-----SDEELKELALRDL 427
DB 424 LRTCVPYSNLDGTGE--AVLLASTYWSQDATR-IGSLVKDAPPQPPKEDLVELILQNL 480
QY 428 AKIHG-----EOVMDKCTGVI-VKKWSADPYSLGAFALFPTPYQHLEYAQELF--SSEGRV 479
DB 481 ARLHAHMTYEKIKEAYTGVIHAYCWANDPNVGGAFALFGPGQFSNLYPYLMRPAAGKFP 540
QY 480 HFAGEHTAFPHAWIETSMKSIRA 503
DB 541 HIVGEASSVHHAWIIGSLESAYTA 564
```

```
RESULT 12
US-09-063-733A-58
; Sequence 58, Application US/09063733A
; Patent No. 6372211
; GENERAL INFORMATION:
; APPLICANT: Isaac, Barbara G.
; APPLICANT: Greenplate, John T.
; APPLICANT: Purcell, John P.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
; NUMBER OF INVENTION: INSECTS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold White & Durkee
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,733A
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
```

```
REFERENCE/DOCKET NUMBER: MOBT:022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-787-1440
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-063-733A-58

Query Match 15.4%; Score 417; DB 3; Length 617;
Best Local Similarity 31.0%; Pred. No. 2.7e-29;
Matches 156; Conservative 83; Mismatches 177; Indels 88; Gaps 26;

QY 62 VVIVGAGMAGLTAALKLQD---AGHTVTILEANDRVGGRVET--YRNEKEGHYAENGAMR 116
DB 87 VCIVGAGVSGLYIAMILDDLKIPNLTYDIFESSRTGGRLYTHHFTDAKHYY-DIGAMR 145
QY 117 ---IPSSHRIVQWFKVLGVEMNEFVMTDDNTFYLVN-----GVRERTYVVQENPDVLK 167
DB 146 YPDIPSMKRTNLP-KRTGMPLIKYLLDGENTPQLYNNHFFAKGVSD-----P 192
QY 168 YNVSESEKISADLLDRALQV-----KEEVEANGCKA--ALEKYDRYSVKYELKBE 218
DB 193 YMVSVANGGTVPDDVVDVSVGEKLQQAFCGYKELAEFDKGFDELMLVDDMTTREVLYKRG 252
QY 219 G--GLSPG---AVRMIGDLLNEQSLMYTALSEMIYDQADVNSV--TYHEVTGSGDLLP 270
DB 253 GPKGEAPKYDFFAIQMMETQNTGTNLFDQAFSEVIDSFDFONPTKPEWYCIEGGTSLLV 312
QY 271 EAFSLVDVPIILLNSKVKHIR----QSDKGIVSVYOTGNESLMDLSADIVLVTITAKAA 326
DB 313 DAMKETLVHKVQNNKRVDAISIDLDPDGG-NMSVRIGGK----DHSGYSTVNTTALGC 367
QY 327 L-----FIDFPPPLISKMEALRSVHYDSSTKILLTFRDKFW-BDDGIR-GGKSITDGP 378
DB 368 LDRMDLRLGLNLHP---TQADAIRCLHYDNSTKVALKFSYPWMIKDCGTCGGAASDLP 423
QY 379 SRYIYYPSSHSP-HTNETIGVLLASTYWSDESLLFLGA-----SDEELKELALRDL 427
DB 424 LRTCVPYSNLDGTGE--AVLLASTYWSQDATR-IGSLVKDAPPQPPKEDLVELILQNL 480
QY 428 AKIHG-----EOVMDKCTGVI-VKKWSADPYSLGAFALFPTPYQHLEYAQELF--SSEGRV 479
DB 481 ARLHAHMTYEKIKEAYTGVIHAYCWANDPNVGGAFALFGPGQFSNLYPYLMRPAAGKFP 540
QY 480 HFAGEHTAFPHAWIETSMKSIRA 503
DB 541 HIVGEASSVHHAWIIGSLESAYTA 564
```

```
RESULT 13
US-09-314-242-2
; Sequence 2, Application US/09314242A
; Patent No. 6248575
; GENERAL INFORMATION:
; APPLICANT: Elizabeth J. Golightly
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
; TITLE OF INVENTION: Having L-Amino Acid Oxidase Activity
; FILE REFERENCE: 5556.200-US
; CURRENT APPLICATION NUMBER: US/09/314,242A
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 09/080,428
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-09-314-242-2
```

Query Match 14.9%; Score 404; DB 3; Length 617;  
Best Local Similarity 30.6%; Pred. No. 4.2e-28;  
Matches 154; Conservative 84; Mismatches 178; Indels 88; Gaps 26;

QY 62 VVVGAGMAGLTAALKLOD---AGHTVILEANDRVGRVET--YRNEKEGYAEMGAMR 116  
DB 87 VCIVGAGVGLYIAMILDKIPNLTYDIFESSRTGRLVTHHPTDAKHYY-DIGAMR 145  
QY 117 ---IPSSHRIQVWFVKLGVENNEFVMTDDNTFYLVN-----GYRETYVVQENPDVLK 167  
DB 146 YPDIFSMKRTFNLF-KRTKMPILIKYLDGENTPOLYNNHFFAKGVSD-----P 192  
QY 168 NVNSESXGISAADLLDRALQKV-----KEEVEANGCKA-ALEKYDRYSVKYLKEE 218  
DB 193 YNVSVANGTVPDDVDSVGEKLAQAFGYKKEKLAEDFKGDELMVLVDDMTREYLKRG 252  
QY 219 G-GLSPG----AVRMIGDLNMQSLMYALSEMITYDOADVNSV--TYHEVTGSGDILLP 270  
DB 253 GPKGEAPKYDFPAIQWMETQNTGTNLFDOAFSESVIDSFDFDNPTKPEWYCIEGTSLLV 312  
QY 271 EAFSLVDVPIILLNSKVHRIH---QSDKGIVSVYQTNESLMDLSADIVLVTAKAA 326  
DB 313 DAMEKTLVHKVQNNKRVDAISIDLDAPDDG-NMSVRIQGGK----EHSGYSTVFNTALGC 367  
QY 327 L-----FIDFPPLSISKMEALRSVHYDSSTKILLTFRDKFW-BDDGIR-GGKSITDGP 378  
DB 368 LDRMDLRGLNHP-----TQADAIRCLHYDNSTKVALKESYPWIKDCGTCGGAASDLP 423  
QY 379 SRIYIYPSHSP-HTNETIGVLASYTWSDESLLFLGA-----SDEBELKELALRDL 427  
DB 424 LRTCVPSYNLADTGE--AVLLASVTWSQDATR-IGSLVKEAPPQPPKEDDELVELILQNL 480  
QY 428 AKIHG-----EQVMDKCTGVI-VKWSADPYSGLGAFALFTPYQHLEYAQELF--SSEGRV 479  
DB 481 ARLHAHMTYKIKAYTGTVHAYCWANDPNVGGAFALFGPGQFNSLNYLYLMPRAAGKGF 540  
QY 480 HFAGHTAPPHAWIETSMKSALRA 503  
DB 541 HIVEASSVHVAHWIGSLESAYTA 564

RESULT 14  
US-09-314-242-12  
; Sequence 12, Application US/09314242A  
; Patent No. 6248575  
; GENERAL INFORMATION:  
; APPLICANT: Elizabeth J. Golightly  
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides  
; FILE REFERENCE: Having L-Amino Acid Oxidase Activity  
; CURRENT APPLICATION NUMBER: US/09/314,242A  
; CURRENT FILING DATE: 1999-05-18  
; EARLIER APPLICATION NUMBER: 09/080,428  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 695  
; TYPE: PRT  
; ORGANISM: Trichoderma harzianum  
US-09-314-242-12

Query Match 14.5%; Score 392; DB 3; Length 695;  
Best Local Similarity 27.0%; Pred. No. 6.4e-27;  
Matches 148; Conservative 90; Mismatches 195; Indels 116; Gaps 26;

QY 37 LEDKDYDTLLQTLNGLPHINTSHVVIIVGAGMAGLTAALKIQDAGHT-VTILEANDRVG 95  
DB 160 LEDKE-----ISIVD---VEKAKSKNIAIVGAGMSGLMYLCLTQAGMTNVSIIEGNRLG 212  
QY 96 GRVET-----YRNEKEGYAEMGAMRIP-----SSHRIV----- 124

DB 213 GRVHTEYLSGPPFDYS-----YQEMGPMRFPNTITLGNETYNVSDHQLVQLAEEMNSL 266  
QY 125 QWFVKVLGVENNEFVMTDDNTFYLVNGVRETYVVQENPDV-LKYNVSESEKGISADLL 183  
DB 267 NGHCKNLVSDFIPWYQNSNGLYYDGIK-----NPTGLPPTLAE-----LAANSSL 314  
QY 184 DRALQKVEEVEANGCAALEKYDRY--SVKEYLKE-----EGGLSPGAVRMIGDL 232  
DB 315 --ALTRYSN---NSTKSLSQKVDALPDTDKFLAEMAQNMFKAHADWLSGGLAGLPGDQ 368  
QY 233 LNEOSLMYALSEMITYDOADVNSVT-----YHEVTGSDLLPEAFSLVL 277  
DB 369 WSEFGFVNVLRGSLNDTAFALPALTRGTCTRGCTFPRRRGAIDGGLNRLPLSFHPLV 428  
QY 278 DVPILLNSKVHGI---RQSDKGVI---VSYOTGNESLMDLSADIVLVTAKAALFIDF 331  
DB 429 DNATTLNRRLEAFDAETQKVTLHRSNYSKDSFESS-----EHDYAVIAAFSIVKKWRF 484  
QY 332 DPPLSISK--MEALRSVHYDSSTKILLTFRDKFEW--DDGIRGGKSIT-DGPS-RYIYY 384  
DB 485 SPALDLTAPTLANAIQNLEYTSACKVALEFRTRFWEHLPPQIYVSCSTTSIPGIGSICY 544  
QY 385 PSHSFHNETIGVLLASY-----TWSDESLLFLGASDEBELKELALRDLAKIHGEQ-VMDKC 439  
DB 545 PSYNINGTDPASILASYISGADWGRD---WVSTPEBEHVQYVLNMAAIIHGEELVKQY 601  
QY 440 TGVIVKK-WSADPYSGLGAFALFTPYQHLEYAQELFSSEGRVHFAGEHTAFPHAWIETSMK 498  
DB 602 TQGNRRCKWALDPLESASWASPTVQGHLYLPEYQTRNNLVFVGEHTSYTHAMIASALE 661  
QY 499 SAIRAATNI 507  
DB 662 SGIRGSVQL 670

RESULT 15  
US-09-482-273-266  
; Sequence 266, Application US/09482273  
; Patent No. 6534631  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 71 Human Secreted Proteins  
; FILE REFERENCE: P2030P1  
; CURRENT APPLICATION NUMBER: US/09/482,273  
; CURRENT FILING DATE: 2000-01-13  
; EARLIER APPLICATION NUMBER: PCT/US99/15849  
; EARLIER FILING DATE: 1999-07-14  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,922  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,956  
; EARLIER FILING DATE: 1998-07-15  
; NUMBER OF SEQ ID NOS: 267  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 266  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (123)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-482-273-266

Query Match 14.3%; Score 387; DB 4; Length 212;  
Best Local Similarity 46.9%; Pred. No. 2.7e-27;  
Matches 84; Conservative 25; Mismatches 44; Indels 26; Gaps 6;

QY 341 EALRSVHYDSSTKILLTFRDKFWEDDGIRGGKSITDGPSRYIYVPSHSFHTNETIGVLLA 400  
DB 7 EALRLHYVPATKVLFSRFRPFWEHEHIEGHSNTDRPSRMIFTP-----PPREGALLJJA 61

Qy 401 SYTWSDESLFLGASDEELKELALRDLAKIHG---EQVWDKCTGVIVKKWSADPYSLGAF 457  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 62 SYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGGF 119  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Qy 458 ALFTPYQHLEYAQELFSSE-----GRVHFAGEHTAFPHAWIETSMKSAIRAAATNIN 508  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 120 VVOXP-----ALMQTEKDDWTVPGRIYFAGEHTAYPHGWVETAVKSAALRAAIKIN 170  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |

Search completed: October 4, 2005, 13:48:06  
Job time : 45 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 13:40:50 ; Search time 479 Seconds  
(without alignments)  
1277.735 Million cell updates/sec

Title: US-10-645-094-1

Perfect score: 2703

Sequence: 1 MNLHVVKWKLWSVLITLY.....TNINKVANEESTIETKDEL 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending patents\_AA\_Main.\*

- 1: /cgn2\_6/ptodata/1/paa/PCTUS COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/paa/US06 COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/paa/US07 COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*
- 7: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*
- 8: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*
- 9: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*
- 10: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*
- 11: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*
- 12: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*
- 13: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*
- 14: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 15: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 16: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 17: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 18: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 19: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 20: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 21: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 22: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 23: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 24: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 25: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*
- 26: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 27: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 28: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 29: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 30: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 31: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 32: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 33: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 34: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 35: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 36: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp.\*
- 37: /cgn2\_6/ptodata/1/paa/US60 COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	524	32	US-10-644-142-1
2	2703	100.0	524	32	US-10-644-142A-1
3	2703	100.0	524	32	US-10-645-094-1
4	1063.5	39.3	516	22	US-09-791-537-143961
5	1059.5	39.2	516	22	US-09-791-537-131193
6	1034	38.3	630	22	US-09-791-537-143903
7	1034	38.3	630	24	US-09-938-795A-1
8	999	37.0	567	1	PCT-US02-08123-1068
9	999	37.0	567	1	PCT-US02-08278-1025
10	999	37.0	567	1	PCT-US02-09785-590
11	999	37.0	567	1	PCT-US03-21083-4
12	999	37.0	567	23	US-09-882-636-13
13	999	37.0	567	24	US-09-938-795A-2
14	999	37.0	567	24	US-09-946-374-84
15	999	37.0	567	26	US-10-001-054-24
16	999	37.0	567	26	US-10-006-041A-84
17	999	37.0	567	26	US-10-006-063A-84
18	999	37.0	567	26	US-10-006-116A-84
19	999	37.0	567	26	US-10-006-117A-84
20	999	37.0	567	26	US-10-006-130A-84
21	999	37.0	567	26	US-10-006-172A-84
22	999	37.0	567	26	US-10-006-485A-84
23	999	37.0	567	26	US-10-006-746A-84
24	999	37.0	567	26	US-10-006-768A-84
25	999	37.0	567	26	US-10-006-818A-84
26	999	37.0	567	26	US-10-006-856A-84
27	999	37.0	567	26	US-10-007-194A-84
28	999	37.0	567	26	US-10-007-236A-84
29	999	37.0	567	26	US-10-011-671A-84
30	999	37.0	567	26	US-10-011-692A-84
31	999	37.0	567	26	US-10-011-795A-84
32	999	37.0	567	26	US-10-011-795B-84
33	999	37.0	567	26	US-10-012-064A-84
34	999	37.0	567	26	US-10-012-101B-84
35	999	37.0	567	26	US-10-012-121A-84
36	999	37.0	567	26	US-10-012-137A-84
37	999	37.0	567	26	US-10-012-149A-84
38	999	37.0	567	26	US-10-012-231A-84
39	999	37.0	567	26	US-10-012-237A-84
40	999	37.0	567	26	US-10-012-252A-84
41	999	37.0	567	26	US-10-012-253A-84
42	999	37.0	567	26	US-10-012-754A-84
43	999	37.0	567	26	US-10-012-755A-84
44	999	37.0	567	26	US-10-012-755A-84
45	999	37.0	567	26	US-10-013-430A-84

ALIGNMENTS

RESULT 1  
US-10-644-142-1  
; Sequence 1, Application US/10644142  
; GENERAL INFORMATION:  
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING  
; FILE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS  
; FILE REFERENCE: 4703/OF214  
; CURRENT APPLICATION NUMBER: US/10/644,142  
; CURRENT FILING DATE: 2003-08-20  
; PRIOR APPLICATION NUMBER: US/09/230,388  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: PCT/JP98/02361  
; PRIOR FILING DATE: 1998-05-22  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 524  
; TYPE: PRT

i ORGANISM: Scomber japonicus			
US-10-644-142-1			
Query Match		100.0%; Score 2703; DB 32; Length 524;	
Best Local Similarity		100.0%; Pred. No. 1.1e-246;	
Matches 524; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MNLHVVKWKL SVSVSLITLYSHTVALSKHEHLADCLDKDYDTLLQTLQDAGHTVTILEANDRVGGRVETRYNEKEGWYAEMGAMRIPSS	60
Db	1	MNLHVVKWKL SVSVSLITLYSHTVALSKHEHLADCLDKDYDTLLQTLQDAGHTVTILEANDRVGGRVETRYNEKEGWYAEMGAMRIPSS	60
Qy	61	HVVI V GAGMAGLTA A K L L Q D A G H T V T I L E A N D R V G G R V E T R Y N E K E G W Y A E M G A M R I P S S	120
Db	61	HVVI V GAGMAGLTA A K L L Q D A G H T V T I L E A N D R V G G R V E T R Y N E K E G W Y A E M G A M R I P S S	120
Qy	121	HRI V Q M F V K L G V E N N E F V M T D D N T F Y L V G V R E T Y V V Q E N P D V L K Y N V S E S E K G I S A D	180
Db	121	HRI V Q M F V K L G V E N N E F V M T D D N T F Y L V G V R E T Y V V Q E N P D V L K Y N V S E S E K G I S A D	180
Qy	181	D L L D R A L Q K V K E E V A N G C K A A L E K Y D R Y S V K E Y L K E E G G L S P G A V R M I G D L L N E Q S L M Y	240
Db	181	D L L D R A L Q K V K E E V A N G C K A A L E K Y D R Y S V K E Y L K E E G G L S P G A V R M I G D L L N E Q S L M Y	240
Qy	241	T A L S E M I Y D Q A D V N D S V T Y H E V T G G S D L L P E A F L S V L D P I L L N S K V K H I R Q S D K G V I V S	300
Db	241	T A L S E M I Y D Q A D V N D S V T Y H E V T G G S D L L P E A F L S V L D P I L L N S K V K H I R Q S D K G V I V S	300
Qy	301	Y Q T G N E S S L M D L S A D I V L V T T T A K A A L F I D F D P P L S I S K M E A L R S V H Y D S S T K I L L T F R D	360
Db	301	Y Q T G N E S S L M D L S A D I V L V T T T A K A A L F I D F D P P L S I S K M E A L R S V H Y D S S T K I L L T F R D	360
Qy	361	K F W E D D G I R G K S I T D G P S R Y I Y P S H S P H T N E T I G V L L A S Y T W S D E S L L F L G A S D E E L K	420
Db	361	K F W E D D G I R G K S I T D G P S R Y I Y P S H S P H T N E T I G V L L A S Y T W S D E S L L F L G A S D E E L K	420
Qy	421	E L A L R D L A K I H G B Q W D K C T G V I V K W S A D P Y S L G A F A L F T P Y Q H L E Y A Q E L F S S E G R V H	480
Db	421	E L A L R D L A K I H G B Q W D K C T G V I V K W S A D P Y S L G A F A L F T P Y Q H L E Y A Q E L F S S E G R V H	480
Qy	481	F A G E H T A F P H A W I T E T S M K S A I R A A T N I N K V A N E E S T I E H T K D E L	524
Db	481	F A G E H T A F P H A W I T E T S M K S A I R A A T N I N K V A N E E S T I E H T K D E L	524
RESULT 3			
US-10-645-094-1			
; Sequence 1, Application US/10645094			
; GENERAL INFORMATION:			
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-kee			
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING			
; FILE REFERENCE: 4703/0F214			
; CURRENT APPLICATION NUMBER: US/10/645,094			
; CURRENT FILING DATE: 2003-08-21			
; PRIOR APPLICATION NUMBER: US/09/912,176			
; PRIOR FILING DATE: 2001-07-24			
; PRIOR APPLICATION NUMBER: US 09/230,388			
; PRIOR FILING DATE: 1999-01-22			
; PRIOR APPLICATION NUMBER: PCT/JP98/02261			
; PRIOR FILING DATE: 1998-05-22			
; NUMBER OF SEQ ID NOS: 2			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 524			
; TYPE: PRT			
; ORGANISM: Scomber japonicus			
US-10-645-094-1			
Query Match			
Best Local Similarity			
Matches 524; Conservative			
Qy	1	MNLHVVKWKL SVSVSLITLYSHTVALSKHEHLADCLDKDYDTLLQTLQDAGHTVTILEANDRVGGRVETRYNEKEGWYAEMGAMRIPSS	60
Db	1	MNLHVVKWKL SVSVSLITLYSHTVALSKHEHLADCLDKDYDTLLQTLQDAGHTVTILEANDRVGGRVETRYNEKEGWYAEMGAMRIPSS	60
Qy	61	HVVI V GAGMAGLTA A K L L Q D A G H T V T I L E A N D R V G G R V E T R Y N E K E G W Y A E M G A M R I P S S	120
Db	61	HVVI V GAGMAGLTA A K L L Q D A G H T V T I L E A N D R V G G R V E T R Y N E K E G W Y A E M G A M R I P S S	120
Qy	121	HRI V Q M F V K L G V E N N E F V M T D D N T F Y L V G V R E T Y V V Q E N P D V L K Y N V S E S E K G I S A D	180
Db	121	HRI V Q M F V K L G V E N N E F V M T D D N T F Y L V G V R E T Y V V Q E N P D V L K Y N V S E S E K G I S A D	180

Qy	181	DLLDRLAQKVKEVEANGKAALEKYDYRYSVKEYLKEEGLSPGAVRMI GDLLNEQSLMY 240
Db	181	DLLDRLAQKVKEVEANGKAALEKYDYRYSVKEYLKEEGLSPGAVRMI GDLLNEQSLMY 240
Qy	241	TALSEMIYDQADVNDSVTHVETGSGDLLPEAFLSVLDVPILLNSKVKH IROSDKGVIVS 300
Db	241	TALSEMIYDQADVNDSVTHVETGSGDLLPEAFLSVLDVPILLNSKVKH IROSDKGVIVS 300
Qy	301	YQTGNESIMDL SADI VLVTTTAKAALFIDFOPPLSISKWEALRSVHYDSSFKILLTFRD 360
Db	301	YQTGNESIMDL SADI VLVTTTAKAALFIDFOPPLSISKWEALRSVHYDSSFKILLTFRD 360
Qy	361	KFWEDDGIRGGKSI TDGFSRYIYYPSSHPTNETIGVLLASYTWSDESLLFLGASDEELK 420
Db	361	KFWEDDGIRGGKSI TDGFSRYIYYPSSHPTNETIGVLLASYTWSDESLLFLGASDEELK 420
Qy	421	ELALRDLAKIHGEQVWDKCTGVI VKWSADPSYSLGAFALFTPYQHLEYAQELFSSEGRVH 480
Db	421	ELALRDLAKIHGEQVWDKCTGVI VKWSADPSYSLGAFALFTPYQHLEYAQELFSSEGRVH 480
Qy	481	FAGEHTAPPHAWIETSMKSAPRAATNINKVANEESTIETHKDEL 524
Db	481	FAGEHTAPPHAWIETSMKSAPRAATNINKVANEESTIETHKDEL 524

```

RESULT 4
US-09-791-537-143961
; Sequence 143961, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143961
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Crotalus atrox
US-09-791-537-143961

```

Query Match	39.3%	Score 1063.5	DB 22	Length 516
Best Local Similarity	44.0%	Pred. No. 6e-91		
Matches 218	Conservative 96	Mismatches 169	Indels 13	Gaps 7
Qy	33	LADCLEDDKDYDTLLQTLQDGLPHLNTSHHVYIVVGAGMAGLTAAKLQDAGHTVTVILEAND	92	
Db	25	LEECFREDYDEFFLEIAKNGGUTATSNPKRVIVVGAGMAGLSAAVYVLAGAGHQVTVLEASE	84	
Qy	93	RVGGRVETRYNEKEGWTAEAGMARI PSSHRIYQVFKKLGVEMNEFVMTDNTFYVLNGV	152	
Db	85	RVGGRVETRYR--KKDWYANLGPMLPTKHRIVREYIKFDDLKNEFSEENENAWYFIKVI	142	
Qy	153	RERTYVVOENPDVLKYNVSESEKIGISADDDLRLALQKVKEEVEANGCKAALEKYDRYSVK	212	
Db	143	RKRVRVKNNPGLLEYVPKPSSEEGKSAQLVSVESLRKVVKELKRTNCKYILDKYDVTYSTK	202	
Qy	213	EYLKEEGGLSPGAVRMIGDLLNEOSLXYTALSEMIYQADVNDSVTYHEVTVGGSDLLPEA	272	
Db	203	EYLLKEGNLSPGAVDMIGDLLNEDSGYVVSFIESLKHDDIFGYEKRFDEIVGGMDQLPTS	262	
Qy	273	FLSVL--DVPILLNSKVKHIRQSDKGVIVSYQT--GNESLLMDLSADIVLVTVTTAKAALFI	329	
Db	263	MYBAIKEKVQVHFENARVIEIQONDREATVTVQTSANEMS--SVTADYIVIVCTTSEAARRI	320	
Qy	330	DFDPPPLSKWEALRSVHYDSSTKILLTFRDQKFWEDDGIRGKSGITDGPSPRIYVYPSHSF	389	
Db	321	KFEPPLPKKAHALRSVHYRSGTKIFUTCKKKFWEDDGTGIRGKSTDLTPSPRFIYVYPHNF	380	

Qy	390	HTNETIGVLLASYTWSDESLLFLGASDEELKALRLAKIH---	GEQWMDKCTGVIVVK	446
Dd	381	TSG--VGVIIA-YGIGDDANFFQALDFDKADIVINDLSLIHQLPKEDITTCRPSMIQR		437
Qy	447	WSADPYSYGAFALTPTYQHLEYAQLFSEGRVHFAGEHTAPPHAWIETSMKSIRAATN		506
Dd	438	WSLDKYANGGITTPYQYQFHFESEALTAPFKRIYFAGEYTAQFGHWIDSTIKSGLTAARD		497
Qy	507	INKVANEESTIEHTKD	522	
Dd	498	VNRASENPSSGIHLNSD	513	

```

RESULT 5
US-09-791-537-131193
; Sequence 131193, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE OF INVENTION: 261/210
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 131193
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Crotalus adamanteus
US-09-791-537-131193

```

[illegible]

```
RESULT 6
US-09-791-537-143903
; Sequence 143903, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143903
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-143903

Query Match      38.3%; Score 1034; DB 22; Length 630;
Best Local Similarity 43.5%; Pred. No. 5.3e-88;
Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;

QY 26 ALSLKEHLADCLDEKDYDTLLQTLDNGLPHINTSHHVIVGVGAGMAGLTAAKLLQDAGHTV 85
DB 25 AASSLNPIEKCMEDHDYEQLLKVVTLGLNRTSKPKQVVVGVAGVAAKMLSDAGHKV 84

QY 86 TLEANDRVGGRVETRYNEKEGVAEMGAMRIPSSHRIVQVFWFKVLGVEMNEFVMTDNT 145
DB 85 TLEADNRIGRIFTFRDEKTCWIGELGAMRMPSSHRILHLKLCRTLGLNLQTOYDENT 144

QY 146 FYLVNGVRETYVVOENPDVLKYNVSESEKISADLLDRALQKVKEVEANGCKAALEK 205
DB 145 WTEVHNVKLRNVVVEKMPKELGYLNNRERGHSPEDIYQMALNKAFAKOLKALGCKKAMNK 204

QY 206 YDRYSVKEYLKEGGISPGAVRMIGDLLNEQSLMYTALSEMIYDQADVNDSVTYHEVTGG 265
DB 205 FNKHTLLEYLLEEGNLSRPVQLLGDVNSEGGFFYLSFAEALRAHACLSDRYRSRIVGG 264

QY 266 SDLLPEAFSLVDVPILLNSKVKHIRQSDKGVIVSYQTGNESLMDLSADIVLVTTTAKA 325
DB 265 WDLPRALLSSLSGALLNAPVVSITQGRNDRVHIATSLHSE-KTLTADVLLTASGPA 323

QY 326 ALFIDPDPPLSISKWEALRSVHYDSSTKILLTFRDKFWEDDGIKGGKSIITDGPRIYYP 385
DB 324 LQRITFSPPLTRKQREALRALHYVAASKVFLSFRFPFWHEEHIEGGHSNTRPSRLIFYP 383

QY 386 SHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKIHGE--QVWDKCTGV 442
DB 384 ARGECS-----LLLASVTWSDAAAPFAGLSTQTLRLVLQDVAAHGPVFRMLWDG-RGV 437

QY 443 IVKWSADPYSLGAFALFTPYQHLEYAQELFSSSE-GRVHFAGEHTAFPHAMTSMKSAI 501
DB 438 -VKRWAEDPHSQGGFVVQPPPLYGREADYDWSAPFGRIYFAGEHTALPHGWVETAVKSGL 496

QY 502 RAATNIN 508
DB 497 RAAVRIN 503

RESULT 7
US-09-938-795A-1
; Sequence 1, Application US/09938795A
; GENERAL INFORMATION:
; APPLICANT: CHU, CHARLES CHIYUAN
; APPLICANT: CHAVAN, SANGEETA S.
; APPLICANT: NASON, JAMES M.
; TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN
; FILE REFERENCE: LIJ-9000-US
; CURRENT APPLICATION NUMBER: US/09/938,795A
```

```
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227,818
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-938-795A-1

Query Match      38.3%; Score 1034; DB 24; Length 630;
Best Local Similarity 43.5%; Pred. No. 5.3e-88;
Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;

QY 26 ALSLKEHLADCLDEKDYDTLLQTLDNGLPHINTSHHVIVGVGAGMAGLTAAKLLQDAGHTV 85
DB 25 AASSLNPIEKCMEDHDYEQLLKVVTLGLNRTSKPKQVVVGVAGVAAKMLSDAGHKV 84

QY 86 TLEANDRVGGRVETRYNEKEGVAEMGAMRIPSSHRIVQVFWFKVLGVEMNEFVMTDNT 145
DB 85 TLEADNRIGRIFTFRDEKTCWIGELGAMRMPSSHRILHLKLCRTLGLNLQTOYDENT 144

QY 146 FYLVNGVRETYVVOENPDVLKYNVSESEKISADLLDRALQKVKEVEANGCKAALEK 205
DB 145 WTEVHNVKLRNVVVEKMPKELGYLNNRERGHSPEDIYQMALNKAFAKOLKALGCKKAMNK 204

QY 206 YDRYSVKEYLKEGGISPGAVRMIGDLLNEQSLMYTALSEMIYDQADVNDSVTYHEVTGG 265
DB 205 FNKHTLLEYLLEEGNLSRPVQLLGDVNSEGGFFYLSFAEALRAHACLSDRYRSRIVGG 264

QY 266 SDLLPEAFSLVDVPILLNSKVKHIRQSDKGVIVSYQTGNESLMDLSADIVLVTTTAKA 325
DB 265 WDLPRALLSSLSGALLNAPVVSITQGRNDRVHIATSLHSE-KTLTADVLLTASGPA 323

QY 326 ALFIDPDPPLSISKWEALRSVHYDSSTKILLTFRDKFWEDDGIKGGKSIITDGPRIYYP 385
DB 324 LQRITFSPPLTRKQREALRALHYVAASKVFLSFRFPFWHEEHIEGGHSNTRPSRLIFYP 383

QY 386 SHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKIHGE--QVWDKCTGV 442
DB 384 ARGECS-----LLLASVTWSDAAAPFAGLSTQTLRLVLQDVAAHGPVFRMLWDG-RGV 437

QY 443 IVKWSADPYSLGAFALFTPYQHLEYAQELFSSSE-GRVHFAGEHTAFPHAMTSMKSAI 501
DB 438 -VKRWAEDPHSQGGFVVQPPPLYGREADYDWSAPFGRIYFAGEHTALPHGWVETAVKSGL 496

QY 502 RAATNIN 508
DB 497 RAAVRIN 503

RESULT 8
PCT-US02-08123-1068
; Sequence 1068, Application PC/TUS0208123
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS904PCT
; CURRENT APPLICATION NUMBER: PCT/US02/08123
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 2048
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1068
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
```







```
QY 3 LHWKWLKSVSVLITLYSYHT - VALSLKEHLADCLDKDYDTLLQTLTDLNGLPHINTGSHH 61
; PRIOR FILING DATE: 1998-09-01
Db 6 LHL-----LVLPILLSVASQDWKERSQDPPEKCHQDPDYEQLLKVKVTWGLNRTLKQOR 61
; PRIOR FILING DATE: 1998-09-02
QY 62 VVVGAGMAGLTAALKLODAGHTVITILEANDRVGGRVETYNKEKGVAEMGAMRIPSSH 121
; PRIOR FILING DATE: 1998-09-02
Db 62 VVVGAGVAGLVAALKVLSAGHKVITILEADNRIGGRIFTYRDONTGWIGELGAMRMPSSH 121
; PRIOR FILING DATE: 1998-09-02
QY 122 RIVQFVKVLGVEMNEFVTDNDTYLVNGVRETYVQENPDVLKYNVSESEKISADD 181
; PRIOR FILING DATE: 1998-09-09
Db 122 RILHLCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKPEKLGALRPOEKHSPED 181
; PRIOR FILING DATE: 1998-09-09
QY 182 LLDRLALQKVEBEANGKAALEKDYKSVKEYLKEEGLSPGAVRMIGDLINQEOSLMYT 241
; PRIOR FILING DATE: 1998-09-09
Db 182 IYQMALNQALKDLKALGCKKAMKFERHTLLYLELGEGLNSRPAVOLLDGVNSEDGFFYL 241
; PRIOR FILING DATE: 1998-09-09
QY 242 ALSEMIYQADVNDVSYTHEVTGGSDLLPEAFSLVDVPIILNSKVKHQRSDKGVIVSY 301
; PRIOR FILING DATE: 1998-09-09
Db 242 SPAEALRAHSCLSDRLOYSRIVGGWDLPLRALSSLSGLVILINAPVWMTQCPHVDHVQI 301
; PRIOR FILING DATE: 1998-09-10
QY 302 QTGNES-SLMDLSADIVLVTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360
; PRIOR FILING DATE: 1998-09-10
Db 302 BTSPARNLKVLUADVLTASGPAVKRITFSPPLRMQEARLRLHYVPATKVFSPRR 361
; PRIOR FILING DATE: 1998-09-10
QY 361 KFEWDDGIRGKSIIDGSRYYTYPSPHPTNETIGVLIASVTGSDSELFLGASDEBLK 420
; PRIOR FILING DATE: 1998-09-10
Db 362 PFWREHIEGHSNDRFSRMIFYP-----PPREGALLLASVTGSDAAAFAGLSREAL 416
; PRIOR FILING DATE: 1998-09-10
QY 421 ELALRDLAKIHG---EQWMDKCTGVIVKWSADPYSGLGAFALFTPYOHLHYAQLFSSE- 476
; PRIOR FILING DATE: 1998-09-10
Db 417 RLALDDVAALHGVVVRQLWDG-TGV-VKRWAEQHSQGGFVVQPE-----ALWQTEK 466
; PRIOR FILING DATE: 1998-09-10
QY 477 -----GVHFAGEHTAPPHAWIETSMKSATRAATNN 508
; PRIOR FILING DATE: 1998-09-10
Db 467 DWTVPYGRIFYAGEHTAYPHGVNVTAVKSAURAAIKIN 505
; PRIOR FILING DATE: 1998-09-10
RESULT 14
US-09-946-374-84
; Sequence 84, Application US/09946374
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
```



APPLICANT: Shelton,David  
APPLICANT: Smith,Victoria  
APPLICANT: Watanabe,Colin  
APPLICANT: Wood,William  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
FILE REFERENCE: P3034R1PCT  
CURRENT APPLICATION NUMBER: US/10/001,054  
CURRENT FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/082399  
PRIOR FILING DATE: 1998-04-24  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/085149  
PRIOR FILING DATE: 1998-05-12  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/090691  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/096891  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/096894  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/099803  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100263  
PRIOR FILING DATE: 1998-09-14  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/107783  
PRIOR FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: 60/108849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112420  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/115554  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115558  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/116533  
PRIOR FILING DATE: 1999-01-20  
PRIOR APPLICATION NUMBER: 60/123618  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/131294  
PRIOR FILING DATE: 1999-04-07  
PRIOR APPLICATION NUMBER: 60/140650  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/141037  
PRIOR FILING DATE: 1999-06-23  
PRIOR APPLICATION NUMBER: 60/144758  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/162506  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: 60/170262  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: 60/187202  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: 60/209832  
PRIOR FILING DATE: 2000-06-05  
PRIOR APPLICATION NUMBER: 60/232887  
PRIOR FILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: 09/180997  
PRIOR FILING DATE: 1998-11-19  
PRIOR APPLICATION NUMBER: 09/218517  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 09/284291  
PRIOR FILING DATE: 1999-04-12  
PRIOR APPLICATION NUMBER: 09/380137  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380913  
PRIOR FILING DATE: 1999-09-09  
PRIOR APPLICATION NUMBER: 09/403297  
PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: 09/423741  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: 09/709238  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 09/802706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 09/866034  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 09/872035  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 09/882636  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/924419  
PRIOR FILING DATE: 2001-08-06  
PRIOR APPLICATION NUMBER: 09/927796  
PRIOR FILING DATE: 2001-08-06  
PRIOR APPLICATION NUMBER: 09/929404  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 09/941992  
PRIOR FILING DATE: 2001-08-28  
PRIOR APPLICATION NUMBER: 09/946374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: PCT/US98/18824  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: PCT/US99/00106  
PRIOR FILING DATE: 1999-01-05  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/08615  
PRIOR FILING DATE: 1999-04-20  
PRIOR APPLICATION NUMBER: PCT/US99/12252  
PRIOR FILING DATE: 1999-06-02  
PRIOR APPLICATION NUMBER: PCT/US99/20111  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28551  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28634  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00376  
PRIOR FILING DATE: 2000-01-06  
PRIOR APPLICATION NUMBER: PCT/US00/03565  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/04342  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/06884

```

: PRIOR FILING DATE: 2000-03-15
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: 2000-03-30
: PRIOR APPLICATION NUMBER: PCT/US00/13705
: PRIOR FILING DATE: 2000-05-17
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: PCT/US00/14941
: PRIOR FILING DATE: 2000-05-30
: PRIOR APPLICATION NUMBER: PCT/US00/15264
: PRIOR FILING DATE: 2000-06-02
: PRIOR APPLICATION NUMBER: PCT/US00/22031
: PRIOR FILING DATE: 2000-08-11
: PRIOR APPLICATION NUMBER: PCT/US00/23522
: PRIOR FILING DATE: 2000-08-23
: PRIOR APPLICATION NUMBER: PCT/US00/30873
: PRIOR FILING DATE: 2000-11-10
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: 2000-12-01
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: PCT/US01/06566
: PRIOR FILING DATE: 2001-03-01
: PRIOR APPLICATION NUMBER: PCT/US01/17092
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: PCT/US01/17800
: PRIOR FILING DATE: 2001-06-01
: PRIOR APPLICATION NUMBER: PCT/US01/19692
: PRIOR FILING DATE: 2001-06-20
: PRIOR APPLICATION NUMBER: PCT/US01/21066
: PRIOR FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: PCT/US01/21735
: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: PCT/US01/27099
: PRIOR FILING DATE: 2001-08-29
: NUMBER OF SEQ ID NOS: 91
: SEQ ID NO 24
: LENGTH: 567
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-001-054-24

```

Query Match	37.0%	Score	999;	DB	26;	Length	567;		
Best Local Similarity	41.8%	Pred.	No.9.3e-85;						
Matches	217;	Conservative	99;	Mismatches	171;	Indels	32;	Gaps	9;

  

Qy	3	LHVVKWKLVSUVSLITLIVYSHT-VALSLKEHLADCLDCKDYDTLTQTLTDNGLPHINTSHH	61
Db	6	LHL-----LVLPILLSVASQDWKAERSQDPFEKCMQDDPYEQULKVVTVWGLNRTLKPQR	61
Qy	62	VVIVGAGWAGLTAAKLLQDAGHTVTTILEANDRVGRVETRYNEKEGYAEMGAMRIPSSH	121
Db	62	VIVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGCRIFTYRDQNTGWIGELGAMRMPSHH	121
Qy	122	RIVQWFKVKLGVENNEFWMTDDNTFYLVNGVRERTYUQENPDVLYKNVSESEKISADD	181
Db	122	RILHKLCOGLGLNLTQYDKNTWTEVHEVKLRYVVEKVPKGLGVALRPQEGKHSPE	181
Qy	182	LLDRALQKVEEVEANGCKAALEKYDRYSKEYLKEBGLSPGAVRMIGOLLNEQSLMYT	241
Db	182	IYQWALNQALDKLKCALGCRKAMKFERHTLTLEYLLGEGNLSRPVQLLGDVMSDEGFFYL	241
Qy	242	ALSEMIYQADVDNVSVTYHEVTGSDLLPFAFLSVLDVPILLNSKVGHIRQSDKGIVSVY	301
Db	242	SFAEALRAHSCLSDRLOQSYRIVGWDLLPRALLSSLSGLVLLNAPVVMYMTQGPDHVHVQI	301
Qy	302	QTGNES-SLMDLSADIIVLVTTKAALFIDFPPLSISKMEALRSVHYDSSTKILLTFRD	360
Db	302	ETSPPARNLKVLKADVLLTASGPAVKRIITSPPLRPHMQEALRLHYVATKVFLSFR	361
Qy	361	KFWEDDGI RGKSIITDGPSTYIYYPHSFHTNETIGVLLASYTWSDBSLFLFLGASDEELK	420
Db	362	PFWRHEEIEGHSNTDRPSRMIFYP-----PPREGALLASYTWSDAFAAFAGLSREAL	416

**THIS PAGE BLANK (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 13:56:21 ; Search time 168 Seconds  
(without alignments)  
1294.767 Million cell updates/sec

Title: US-10-645-094-1

Perfect score: 2703

Sequence: 1 MNLHVWKLSVSVSLITLY.....TNINKVANEESTIETKDEL 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2703	100.0	524	9 US-09-912-176-1	Sequence 1, Appli
2	2703	100.0	524	15 US-10-644-142-1	Sequence 1, Appli
3	2703	100.0	524	18 US-10-645-094-1	Sequence 1, Appli
4	1034	38.3	630	10 US-09-938-795A-1	Sequence 1, Appli
5	999	37.0	567	10 US-09-938-795A-2	Sequence 2, Appli
6	999	37.0	567	10 US-09-946-374-84	Sequence 84, Appli
7	999	37.0	567	13 US-10-001-054-24	Sequence 24, Appli
8	999	37.0	567	13 US-10-053-107-2	Sequence 2, Appli
9	999	37.0	567	14 US-10-028-072-476	Sequence 476, App
10	999	37.0	567	14 US-10-140-808-476	Sequence 476, App
11	999	37.0	567	14 US-10-121-049-476	Sequence 476, App

ALIGNMENTS

RESULT 1  
US-09-912-176-1  
; Sequence 1, Application US/09912176  
; Patent No. US20020034804A1  
; GENERAL INFORMATION:  
; APPLICANT: Iwanoto, Mitsunori; Jung, Sang-Ke  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING  
; FILE REFERENCE: 4703/0F214  
; CURRENT APPLICATION NUMBER: US/09/912.176  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR FILING DATE: 2001/07/24  
; PRIOR APPLICATION NUMBER: US 09/230,388  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: PCT/JF98/02261  
; PRIOR FILING DATE: 1998-05-22  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 524  
; TYPE: PRT  
; ORGANISM: Scomber japonicus  
US-09-912-176-1

Query Match 100.0%; Score 2703; DB 9; Length 524;  
Best Local Similarity 100.0%; Pred. No. 1.3e-216;  
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNLHVWKLSVSVSLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNGLPHINTSH 60  
Db 1 MNLHVWKLSVSVSLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNGLPHINTSH 60  
Qy 61 HWIVGAGMAGLTAALKLQDAGHTVTILEANDRVGGRVETVYRNEKEGWAEMGARIPSS 120

Db 61 HVIIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGWAEMGAMRIPSS 120  
Qy 121 HRIVQWFKVLGVENNEFWMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKGISAD 180  
Db 121 HRIVQWFKVLGVENNEFWMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKGISAD 180  
Qy 181 DLLDRALQVKVEVEANGKAALEKYDRYSVKEYLKEGGISPGAVRMIGDILLNQSLMY 240  
Db 181 DLLDRALQVKVEVEANGKAALEKYDRYSVKEYLKEGGISPGAVRMIGDILLNQSLMY 240  
Qy 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVDVPIILLNSKVKHIRQSDKGIVTS 300  
Db 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVDVPIILLNSKVKHIRQSDKGIVTS 300  
Qy 301 YQTGNESLMDLSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360  
Db 301 YQTGNESLMDLSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360  
Qy 361 KFWEDDGIRGKSIITDGPSTYIYPSHSPHTNETIGVLLASYTWSDESLLFLGASDEBLK 420  
Db 361 KFWEDDGIRGKSIITDGPSTYIYPSHSPHTNETIGVLLASYTWSDESLLFLGASDEBLK 420  
Qy 421 ELALRDLAKIHGEQVWDKCTGVIIVKWSADPYSLGAFALFTPYQHLEVAQELFSSEGRVH 480  
Db 421 ELALRDLAKIHGEQVWDKCTGVIIVKWSADPYSLGAFALFTPYQHLEVAQELFSSEGRVH 480  
Qy 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIHTKDEL 524  
Db 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIHTKDEL 524

## RESULT 2

US-10-644-142-1  
; Sequence 1, Application US/10644142  
; Publication No. US20040054147A1  
; GENERAL INFORMATION:  
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING  
; FILE REFERENCE: 4703/0F214  
; CURRENT APPLICATION NUMBER: US/10/644,142  
; PRIOR FILING DATE: 2003-08-20  
; PRIOR APPLICATION NUMBER: US/09/230,388  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: PCT/JP98/02261  
; PRIOR FILING DATE: 1998-05-22  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; TYPE: PRT  
; LENGTH: 524  
; ORGANISM: Scomber japonicus  
US-10-644-142-1

Query Match 100.0%; Score 2703; DB 15; Length 524;  
Best Local Similarity 100.0%; Pred. No. 1.3e-216;  
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNLHVVKWKLSSVSVLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSH 60  
Db 1 MNLHVVKWKLSSVSVLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSH 60  
Qy 61 HVIIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGWAEMGAMRIPSS 120  
Db 61 HVIIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGWAEMGAMRIPSS 120  
Qy 121 HRIVQWFKVLGVENNEFWMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKGISAD 180  
Db 121 HRIVQWFKVLGVENNEFWMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKGISAD 180  
Qy 181 DLLDRALQVKVEVEANGKAALEKYDRYSVKEYLKEGGISPGAVRMIGDILLNQSLMY 240  
Db 181 DLLDRALQVKVEVEANGKAALEKYDRYSVKEYLKEGGISPGAVRMIGDILLNQSLMY 240

Qy 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVDVPIILLNSKVKHIRQSDKGIVTS 300  
Db 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVDVPIILLNSKVKHIRQSDKGIVTS 300  
Qy 301 YQTGNESLMDLSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360  
Db 301 YQTGNESLMDLSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360  
Qy 361 KFWEDDGIRGKSIITDGPSTYIYPSHSPHTNETIGVLLASYTWSDESLLFLGASDEBLK 420  
Db 361 KFWEDDGIRGKSIITDGPSTYIYPSHSPHTNETIGVLLASYTWSDESLLFLGASDEBLK 420  
Qy 421 ELALRDLAKIHGEQVWDKCTGVIIVKWSADPYSLGAFALFTPYQHLEVAQELFSSEGRVH 480  
Db 421 ELALRDLAKIHGEQVWDKCTGVIIVKWSADPYSLGAFALFTPYQHLEVAQELFSSEGRVH 480  
Qy 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIHTKDEL 524  
Db 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIHTKDEL 524

## RESULT 3

US-10-645-094-1  
; Sequence 1, Application US/10645094  
; Publication No. US20050191737A1  
; GENERAL INFORMATION:  
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING  
; FILE REFERENCE: 4703/0F214  
; CURRENT APPLICATION NUMBER: US/10/645,094  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR FILING DATE: US/09/912,176  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: US 09/230,388  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: PCT/JP98/02261  
; PRIOR FILING DATE: 1998-05-22  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; TYPE: PRT  
; LENGTH: 524  
; ORGANISM: Scomber japonicus  
US-10-645-094-1

Query Match 100.0%; Score 2703; DB 18; Length 524;  
Best Local Similarity 100.0%; Pred. No. 1.3e-216;  
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNLHVVKWKLSSVSVLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSH 60  
Db 1 MNLHVVKWKLSSVSVLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSH 60  
Qy 61 HVIIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGWAEMGAMRIPSS 120  
Db 61 HVIIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGWAEMGAMRIPSS 120  
Qy 121 HRIVQWFKVLGVENNEFWMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKGISAD 180  
Db 121 HRIVQWFKVLGVENNEFWMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKGISAD 180  
Qy 181 DLLDRALQVKVEVEANGKAALEKYDRYSVKEYLKEGGISPGAVRMIGDILLNQSLMY 240  
Db 181 DLLDRALQVKVEVEANGKAALEKYDRYSVKEYLKEGGISPGAVRMIGDILLNQSLMY 240  
Qy 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVDVPIILLNSKVKHIRQSDKGIVTS 300  
Db 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVDVPIILLNSKVKHIRQSDKGIVTS 300  
Qy 301 YQTGNESLMDLSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360  
Db 301 YQTGNESLMDLSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360

Db 301 YQTGNESSLMDLSADIVLVTTTAKAALFIDFDPPLSISKWEALRSVHYDSSTKILLTFRD 360  
Qy 361 KFWEDDGIRGKSITDGPRIYIYPSPHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420  
Db 361 KFWEDDGIRGKSITDGPRIYIYPSPHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420  
Qy 421 ELALRDLAKIHGEQWWDKCTGVIVKWSADPYSLGAFALFTPYQHLEVAQELFSSEGRVH 480  
Db 421 ELALRDLAKIHGEQWWDKCTGVIVKWSADPYSLGAFALFTPYQHLEVAQELFSSEGRVH 480  
Qy 481 FAGEHTAFPHAMTETSMKSAIRAATNINKVANEESTIETHTKDEL 524  
Db 481 FAGEHTAFPHAMTETSMKSAIRAATNINKVANEESTIETHTKDEL 524

RESULT 4  
US-09-938-795A-1  
; Sequence 1, Application US/09938795A  
; Publication No. US20030045688A1  
; GENERAL INFORMATION:  
; APPLICANT: CHU, CHARLES CHIYUAN  
; APPLICANT: CHAVAN, SANGEETA S.  
; APPLICANT: MASON, JAMES M.  
; TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN  
; FILE REFERENCE: LIJ-9000-US  
; CURRENT APPLICATION NUMBER: US/09/938,795A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/227,818  
; PRIOR FILING DATE: 2000-08-25  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-938-795A-1

Query Match 38.3%; Score 1034; DB 10; Length 630;  
Best Local Similarity 43.5%; Pred. No. 3,9e-77;  
Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;  
Qy 26 ALSLKEHLADCLDEDKYDTLLQTLONGPLPHINTSHHVIIVGAGMAGLTAAKLLQDAGHTV 85  
Db 25 AASSLNPIEKCMEDHDYEQLLKVTLLGLNRTSKPKQVYVVGAGVAGLVAAKMLSDAGHKV 84  
Qy 86 TLEANDRVGGRTVETRYNEKEGYAEWGAMRTPSSSHRIYQWVFVKLGVMNEFVMTDNT 145  
Db 85 TLEADNRIGGRIFTRDEKTMIGELGAMRWPSSHRILHKL CRTLGMLTQFTQYDENT 144  
Qy 146 FYLVNGVRERTYVVOENPDVLKYNVSESEKGISADLLDLRALQKVKEEVEANGKAALEK 205  
Db 145 MTEVHNVLKRNIVVEKMPKCYLNNRERHSPEDIYQMALNKAFKDLKALGCKKAMNK 204  
Qy 206 YDRYSVKEVKEEGGLSPGAVRMIGDLINEQSLMTALSEMIYDQADVNDVSYHYEVTGG 265  
Db 205 FNKHTLLEYLLBEGNLSRPAVQLLGDVMSEEGFFYLSFAEALRAHACLSRLRYSRIVGG 264  
Qy 266 SLLPEAFSLVDVPTLLNSKVKHROSQDKGIVSVQTGNESSLMDLSADIVLVTTTAKA 325  
Db 265 WDLPRALLUSSGALLNAPVVSITQGRNDRVHIATSLHSE-KTLTADVLLTASGPA 323  
Qy 326 ALFIDFDPPLSLSKMEALRSVHYDSSTKILLTFRDKFWEDDGIRGKSITDGPRIYIYP 385  
Db 324 LQRIITFSPPLTRKQERQALRALHYVAASKVFLSFRFPFWHEEHI EGGHNSNDRPSRLIFYP 383  
Qy 386 SHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKIHGE---QVWDKCTGV 442  
Db 384 ARGEKS-----LLLASYTWSDAAPFAGLSLTDQTLRLVLQDVAALHGPVVFRLWDG-RGV 437  
Qy 443 IVKWSADPYSLGAFALFTPYQHLEVAQELFSSE-GRVHFACEHTAFPHAMTETSMKSAI 501  
Db 438 -VKRWAEDPHSGGFWOPPLYGREAEVDWSAPFGRIFYFAGEHTALPHGWVETAVKSGL 496

Qy 502 RAATNIN 508  
Db 497 RAAVRIN 503

RESULT 5  
US-09-938-795A-2  
; Sequence 2, Application US/09938795A  
; Publication No. US20030045688A1  
; GENERAL INFORMATION:  
; APPLICANT: CHU, CHARLES CHIYUAN  
; APPLICANT: CHAVAN, SANGEETA S.  
; APPLICANT: MASON, JAMES M.  
; TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN  
; FILE REFERENCE: LIJ-9000-US  
; CURRENT APPLICATION NUMBER: US/09/938,795A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/227,818  
; PRIOR FILING DATE: 2000-08-25  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-938-795A-2

Query Match 37.0%; Score 999; DB 10; Length 567;  
Best Local Similarity 41.8%; Pred. No. 2.8e-74;  
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;  
Qy 3 LHVVKWKL SVSVLITLYYSHT-VALSLKEHLADCLDEDKYDTLLQTLONGPLPHINTSHH 61  
Db 6 LHL-----LVLVPIILSLVASQDQWKAERSQSDPEKCKWQPDYEQLLKVVWTGLNRTLKPQR 61  
Qy 62 VVIVGAGMAGLTAAKLLQDAGHTVITLEANDRVGGRTVETRYNEKEGYAEWGAMRIPSSH 121  
Db 62 VVIVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRQNTGTWIGELGAMRMPSSH 121  
Qy 122 RIVQWVFVKLGVMNEFVMTDNTFVLNGVRERTYVVOENPDVLKYNVSESEKGISADD 181  
Db 122 RILHKLCOGLGULNLTFTQYDKNTWTEVHEVKLRNVYVEKVKUGYALRPOEKHSPED 181  
Qy 182 LDLRALQKVKEEVEANGKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLINEQSLMT 241  
Db 182 IYQMALNQALKDLKALGCKKAMKKEFHTLLEYLLGEGNLSRPAVQLLGDVMSDGFYFL 241  
Qy 242 ALSEMIYDQADVNDVSYHYEVTGGSDLLPEAFSLVDVPTLLNSKVKHROSQDKGIVSY 301  
Db 242 SFAEALRAHSCLSRLRYSRIVGGWDLPLRALLSLSGLVLLNAPVVAWMTQGPHDVHVOI 301  
Qy 302 QTGNES-SLMDLSADIVLVTTTAKAALFIDPPLSISKWEALRSVHYDSSTKILLTFRD 360  
Db 302 ETSPPARNLKVLDKADVLLTASGPAVKRITPSPPLRHMQEARLRHLHYVPATKVFLSFR 361  
Qy 361 KFWEDDGIRGKSITDGPRIYIYPSPHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420  
Db 362 PFWHEEHIEGHSNDRPSRLIFYP-----PPREGALLASYTWSDAFAAFAGLSREAL 416  
Qy 421 ELALRDLAKIHGE---EQWWDKCTGVIVKWSADPYSLGAFALFTPYQHLEVAQELFSSE- 476  
Db 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEDQHSQSGFVVQPP-----ALMQTEK 466  
Qy 477 -----GRVHFACEHTAFPHAMTETSMKSAIRAATNIN 508  
Db 467 DDWTVPGRIYFAGEHTAYPHGWTAVKSLRAAIAIKIN 505

RESULT 6  
US-09-946-374-84  
; Sequence 84, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geo, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30



; PRIOR APPLICATION NUMBER: 60/108849  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 60/112420  
; PRIOR FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: 60/113296  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 60/115554  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/115558  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/116533  
; PRIOR FILING DATE: 1999-01-20  
; PRIOR APPLICATION NUMBER: 60/123618  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: 60/131294  
; PRIOR FILING DATE: 1999-04-07  
; PRIOR APPLICATION NUMBER: 60/140650  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: 60/141037  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 60/144758  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/162506  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: 60/170262  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: 60/187202  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/209832  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: 60/232887  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 09/180997  
; PRIOR FILING DATE: 1998-11-19  
; PRIOR APPLICATION NUMBER: 09/218517  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 09/284291  
; PRIOR FILING DATE: 1999-04-12  
; PRIOR APPLICATION NUMBER: 09/380137  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: 09/380138  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: 09/380913  
; PRIOR FILING DATE: 1999-09-09  
; PRIOR APPLICATION NUMBER: 09/403297  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: 09/423741  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: 09/709238  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 09/802706  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 09/866034  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 09/872035  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: 09/882636  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 09/924419  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/927796  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/929404  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: 09/941992  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 09/946374  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: PCT/US98/18824  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: PCT/US99/00106

; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: PCT/US99/05028  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: PCT/US99/08615  
; PRIOR FILING DATE: 1999-04-20  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: PCT/US99/20111  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28551  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28634  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00376  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: PCT/US00/04341  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04342  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: PCT/US00/06884  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/US00/13705  
; PRIOR FILING DATE: 2000-05-17  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: PCT/US00/14941  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: PCT/US00/22031  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: PCT/US00/23522  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: PCT/US00/30873  
; PRIOR FILING DATE: 2000-11-10  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: PCT/US01/06666  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: PCT/US01/17092  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: PCT/US01/17800  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19692  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: PCT/US01/21066  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/21735  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: PCT/US01/27099  
; PRIOR FILING DATE: 2001-08-29  
; NUMBER OF SEQ ID NOS: 91  
; SEQ ID NO 24  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-001-054-24

```
Query Match 37.0%; Score 999; DB 13; Length 567;
Best Local Similarity 41.8%; Pred. No. 2.8e-74;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVVKVSVVSVLITLYSHT-VALSLKEHLADCLDXYDTLLQTLONGLPHINTSHH 61
Db 6 LHL-----LVLVPIILLSVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPOR 61

Qy 62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETRYNEKEGWYAEKMGAMRIPSSH 121
Db 62 VVIVGAGVAGLVAAKVLSDAGHKVTILEADNRIGRIFFYRDQNTGWIGELGMMRPPSH 121

Qy 122 RIVQFVKKLVGEMNEFVMTDNTFYLNGVRERTYVVOENPDVLKYNVSESEKGISADD 181
Db 122 RILHLKCOGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKPEKLGVALRPOEKHSPED 181

Qy 182 LLDRLALQKVEEVEANGCKAALEKYDRYSVKEYLKEEGLSPGAVRMIGDLNBOSLMYT 241
Db 182 IYQMALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLDGVMSDEGFFYL 241

Qy 242 ALSEMIYDQADVNDSTVYHEVTGGSDLLPEAFSLVDVPIILLNSKVKHIRQSDKGVISY 301
Db 242 SFAEALRAHSCUSDRLQYSRIVGGWDLPRALLSSGLVLLNAPVAMTQGHVDHVOI 301

Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFPPPLSISKWEALRSVHYDSSTKILLTFRD 360
Db 302 ETSPPARNLKVLDVLLTASGPAVKRITFPPLPRHQEALRLHYVPATKVFLSFR 361

Qy 361 KFWEDDGIKGGKSTIDGPRSRIYYPSHSHFHTNETGVLLASVTSDESLLFLGASDEULK 420
Db 362 PFWREHIEGGHNSNTRDPSRMIFYP-----PPREGALLASVTSDDAAAFAAGLSREAL 416

Qy 421 ELALRDLAKIHG---EOWDKCTGVIVKWSADPVSGLGAFALFTFVQHLEYAQELPSSB- 476
Db 417 RLALDDVAAALRGVVRVQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALWQTEK 466

Qy 477 -----GRVHPAGEHTAPPHAWIETSMKSASIRAAATNIN 508
Db 467 DDMVTVPYGRHYPAGEHTAVPHGMVETAVKSAIRAIAKIN 505

RESULT 8
US-10-053-107-2
; Sequence 2, Application US/10053107
; Publication No. US20020192752A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P3033R1C1
; CURRENT APPLICATION NUMBER: US/10/053,107
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/099601
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/107783
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/108802
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
```

```
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/218517
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US99/00106
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/13705
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 2
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-053-107-2

Query Match 37.0%; Score 999; DB 13; Length 567;
Best Local Similarity 41.8%; Pred. No. 2.8e-74;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVVKVSVVSVLITLYSHT-VALSLKEHLADCLDXYDTLLQTLONGLPHINTSHH 61
Db 6 LHL-----LVLVPIILLSVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPOR 61

Qy 62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETRYNEKEGWYAEKMGAMRIPSSH 121
Db 62 VVIVGAGVAGLVAAKVLSDAGHKVTILEADNRIGRIFFYRDQNTGWIGELGMMRPPSH 121

Qy 122 RIVQFVKKLVGEMNEFVMTDNTFYLNGVRERTYVVOENPDVLKYNVSESEKGISADD 181
Db 122 RILHLKCOGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKPEKLGVALRPOEKHSPED 181

Qy 182 LLDRLALQKVEEVEANGCKAALEKYDRYSVKEYLKEEGLSPGAVRMIGDLNBOSLMYT 241
Db 182 IYQMALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLDGVMSDEGFFYL 241

Qy 242 ALSEMIYDQADVNDSTVYHEVTGGSDLLPEAFSLVDVPIILLNSKVKHIRQSDKGVISY 301
Db 242 SFAEALRAHSCUSDRLQYSRIVGGWDLPRALLSSGLVLLNAPVAMTQGHVDHVOI 301

Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFPPPLSISKWEALRSVHYDSSTKILLTFRD 360
Db 302 ETSPPARNLKVLDVLLTASGPAVKRITFPPLPRHQEALRLHYVPATKVFLSFR 361

Qy 361 KFWEDDGIKGGKSTIDGPRSRIYYPSHSHFHTNETGVLLASVTSDESLLFLGASDEULK 420
Db 362 PFWREHIEGGHNSNTRDPSRMIFYP-----PPREGALLASVTSDDAAAFAAGLSREAL 416

Qy 421 ELALRDLAKIHG---EOWDKCTGVIVKWSADPVSGLGAFALFTFVQHLEYAQELPSSB- 476
Db 417 RLALDDVAAALRGVVRVQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALWQTEK 466

Qy 477 -----GRVHPAGEHTAPPHAWIETSMKSASIRAAATNIN 508
Db 467 DDMVTVPYGRHYPAGEHTAVPHGMVETAVKSAIRAIAKIN 505
```





```
Qy 3 LHVWKVSVSVLITLYSHT - VALSLKEHLADCLEDKDYDTLLQTLNDGLPHINTSHH 61
Db 6 LHL-----LVLPILLSVASQDKAERSQDPPEKCMQDPDYEQLLKVVWGLNRTLKQOR 61

Qy 62 VVIVGAGMAGLTAALKLODAGHTVTILEANDRVGGRVETRYNEKEGYAEMGAMRIPSSH 121
Db 62 VVIVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGIGELGAMRMPSSH 121

Qy 122 RIVQFVKVLGVEMNEFVMTDNTFYLVNGVRERYVVOENPDVLKYNVSESEKISADD 181
Db 122 RILHKLCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVYVEKPEKLGVALRPOEKHSPED 181

Qy 182 LLDRALOKVKEVEANGCKAALKEDRYSVKEYLKEEGSLSPGAVRMIGDLNOSLMYT 241
Db 182 IYQMALNQALKDLKALGCKAMKFERHTLLEYLLGEGNLSRPAVQLLDGVMSDGFYL 241

Qy 242 ALSEMIYQADVNDVSVTYHEVTGGDLPEAFSLVDVPIILNSKVKHRSQDKGVIVSY 301
Db 242 SFAALRAHSCSLDRLOYSRIVGGWDLPLRALLSSLSGLVLLNAPVAVMTQCPHDVHVOI 301

Qy 302 QTGNES-SLMDLSADIVLVTTAKAALFIDPDPPLSISKMEALRSVHYDSSTKILLTFRD 360
Db 302 ETSPPARNLKVLDVLLTASGPAVKRITFSPPLPRHMQEALRLHYVPATKVPFLSPRR 361

Qy 361 KFWEDDGIRGKSIIDGSPRYIYPSHSFHTNETIGVLILASYTWSDESLLFLGASDEBK 420
Db 362 PFWREHIEGHSNTDRPSRMIFYP-----PPREGALLASYTWSDAAGLRSREAL 416

Qy 421 ELALRDLAKIHG---EQVWDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQLFSSE- 476
Db 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGFVVQPP-----ALWQTEK 466

Qy 477 -----GRVHFACEHTAFPHAWIETSMKSAIRAATNIN 508
Db 467 DDWTPVYGRIFYFAGEHTAYPHGWVETAVKSAURAAIKIN 505
```

## RESULT 11

```
US-10-121-049-476
; Sequence 476, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33301C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 476
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-476
```

Query Match 37.0%; Score 999; DB 14; Length 567;

```
Best Local Similarity 41.8%; Pred. No. 2.8e-74;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVWKVSVSVLITLYSHT - VALSLKEHLADCLEDKDYDTLLQTLNDGLPHINTSHH 61
Db 6 LHL-----LVLPILLSVASQDKAERSQDPPEKCMQDPDYEQLLKVVWGLNRTLKQOR 61

Qy 62 VVIVGAGMAGLTAALKLODAGHTVTILEANDRVGGRVETRYNEKEGYAEMGAMRIPSSH 121
Db 62 VVIVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGIGELGAMRMPSSH 121

Qy 122 RIVQFVKVLGVEMNEFVMTDNTFYLVNGVRERYVVOENPDVLKYNVSESEKISADD 181
Db 122 RILHKLCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVYVEKPEKLGVALRPOEKHSPED 181

Qy 182 LLDRALOKVKEVEANGCKAALKEDRYSVKEYLKEEGSLSPGAVRMIGDLNOSLMYT 241
Db 182 IYQMALNQALKDLKALGCKAMKFERHTLLEYLLGEGNLSRPAVQLLDGVMSDGFYL 241

Qy 242 ALSEMIYQADVNDVSVTYHEVTGGDLPEAFSLVDVPIILNSKVKHRSQDKGVIVSY 301
Db 242 SFAALRAHSCSLDRLOYSRIVGGWDLPLRALLSSLSGLVLLNAPVAVMTQCPHDVHVOI 301

Qy 302 QTGNES-SLMDLSADIVLVTTAKAALFIDPDPPLSISKMEALRSVHYDSSTKILLTFRD 360
Db 302 ETSPPARNLKVLDVLLTASGPAVKRITFSPPLPRHMQEALRLHYVPATKVPFLSPRR 361

Qy 361 KFWEDDGIRGKSIIDGSPRYIYPSHSFHTNETIGVLILASYTWSDESLLFLGASDEBK 420
Db 362 PFWREHIEGHSNTDRPSRMIFYP-----PPREGALLASYTWSDAAGLRSREAL 416

Qy 421 ELALRDLAKIHG---EQVWDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQLFSSE- 476
Db 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGFVVQPP-----ALWQTEK 466

Qy 477 -----GRVHFACEHTAFPHAWIETSMKSAIRAATNIN 508
Db 467 DDWTPVYGRIFYFAGEHTAYPHGWVETAVKSAURAAIKIN 505
```

## RESULT 12

```
US-10-123-904-476
; Sequence 476, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33301C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 476
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo Sapien
```

US-10-123-904-476

```
Query Match 37.0%; Score 999; DB 14; Length 567;
Best Local Similarity 41.8%; Pred. No. 2.8e-74;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVVKVKSLSVSVLITLYSHT-VALSLKEHLADCLDEKDYDTLLQTLQDGLPHINTSHH 61
DB 6 LHL-----LVLVPILLSLVASQDWKAERSQDPPEKCMQDDPYEQLLKVVWGLNRTLKPOR 61
QY 62 VIVVGAGMAGLTAALKLQDAGHTVTILEANDRVGRVETRYNEKEGKGYAEMGAMRIPSSH 121
DB 62 VIVVGAGVAGLVAARKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSH 121
QY 122 RIVQFVKVLGVEMNEFVMTDNTFYLVNGVRERTYVVOENPDVLKYNVSESEKGISADD 181
DB 122 RILHLKCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKPEKLGALRPOEKGHSPED 181
QY 182 LLDRLAQKVEEVEANGCAALEKYDRYSVKEYLKEEGSLSPGAVRMIGDLLNEOSLMYT 241
DB 182 IYQMALNQALKDLKALGCRKAMKPERHTLLEYLLGEGNLSRPVQLLDVMSDGFYFL 241
QY 242 ALSEMIYQADVNDVSVTYHEVTGSGDLLPEAFSLVLDVPILLNSKVXGHRQSDKGVIVSY 301
DB 242 SFAEALRAHSCUSDRLQYSRIVGGWDLPLRALLSSLSGLVLLNAPVAMTQCPHDVHVOI 301
QY 302 QTGNES-SLMOLSDADIVLTTAKAALFIDFPPPLSISKMEALRSVHYDSSTKILLTFRD 360
DB 302 ETSPPARNLKVLDVLLTASGPAVKRITFPSPPLRHMQLRRLHYVPATKVFLSFR 361
QY 361 KFWEDDGRGKSIITDGPRIYIYPSHSHFHTNETIGVLLASVTWDESLLFLGASDEELK 420
DB 362 PFWRBEHTEGGHSNDRPSRMIFYP-----PPREGALLLASVTWSDAAAFAAGLSREAL 416
QY 421 ELALDLAKIHG---EQWDKCTGVIVKWSADPVSGLGAFALFTPYQHLEVAQELFSSB- 476
DB 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEDQHSQGFVVQPP-----ALWQTEK 466
QY 477 -----GRVHFAEHTAPPHAWIETSMKSAIRAATNIN 508
DB 467 DDMTVPYGRIVYAGEHTAYPHGWVETAVKSALRAAIKIN 505
```

```
RESULT 13
US-10-140-470-476
; Sequence 476, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 476
```

```
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-476

Query Match 37.0%; Score 999; DB 14; Length 567;
Best Local Similarity 41.8%; Pred. No. 2.8e-74;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVVKVKSLSVSVLITLYSHT-VALSLKEHLADCLDEKDYDTLLQTLQDGLPHINTSHH 61
DB 6 LHL-----LVLVPILLSLVASQDWKAERSQDPPEKCMQDDPYEQLLKVVWGLNRTLKPOR 61
QY 62 VIVVGAGMAGLTAALKLQDAGHTVTILEANDRVGRVETRYNEKEGKGYAEMGAMRIPSSH 121
DB 62 VIVVGAGVAGLVAARKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSH 121
QY 122 RIVQFVKVLGVEMNEFVMTDNTFYLVNGVRERTYVVOENPDVLKYNVSESEKGISADD 181
DB 122 RILHLKCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKPEKLGALRPOEKGHSPED 181
QY 182 LLDRLAQKVEEVEANGCAALEKYDRYSVKEYLKEEGSLSPGAVRMIGDLLNEOSLMYT 241
DB 182 IYQMALNQALKDLKALGCRKAMKPERHTLLEYLLGEGNLSRPVQLLDVMSDGFYFL 241
QY 242 ALSEMIYQADVNDVSVTYHEVTGSGDLLPEAFSLVLDVPILLNSKVXGHRQSDKGVIVSY 301
DB 242 SFAEALRAHSCUSDRLQYSRIVGGWDLPLRALLSSLSGLVLLNAPVAMTQCPHDVHVOI 301
QY 302 QTGNES-SLMOLSDADIVLTTAKAALFIDFPPPLSISKMEALRSVHYDSSTKILLTFRD 360
DB 302 ETSPPARNLKVLDVLLTASGPAVKRITFPSPPLRHMQLRRLHYVPATKVFLSFR 361
QY 361 KFWEDDGRGKSIITDGPRIYIYPSHSHFHTNETIGVLLASVTWDESLLFLGASDEELK 420
DB 362 PFWRBEHTEGGHSNDRPSRMIFYP-----PPREGALLLASVTWSDAAAFAAGLSREAL 416
QY 421 ELALDLAKIHG---EQWDKCTGVIVKWSADPVSGLGAFALFTPYQHLEVAQELFSSB- 476
DB 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEDQHSQGFVVQPP-----ALWQTEK 466
QY 477 -----GRVHFAEHTAPPHAWIETSMKSAIRAATNIN 508
DB 467 DDMTVPYGRIVYAGEHTAYPHGWVETAVKSALRAAIKIN 505
```

```
RESULT 14
US-10-175-746-476
; Sequence 476, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 13:48:15 ; Search time 43 Seconds  
(without alignments)  
1172.502 Million cell updates/sec

Title: US-10-645-094-1  
Perfect score: 2703  
Sequence: 1 MNLHVVKWKLVSVLITLY.....TNINKVANEESTIHTKDEL 524

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1059.5	39.2	516	2 JE0266	L-amino-acid oxida
2	1055.5	39.0	516	2 JC8015	L-amino-acid oxida
3	737.5	27.3	446	2 E69899	L-amino acid oxida
4	641	23.7	701	2 JC8062	L-glutamate oxidas
5	412	15.2	526	2 A75581	flavin monoamine o
6	392	14.5	426	2 A12498	L-amino acid oxida
7	392	14.5	695	2 A38114	L-amino-acid oxida
8	383.5	14.2	541	2 A87595	amine oxidase, fla
9	353.5	13.1	534	2 G87384	amine oxidase, fla
10	307	11.4	496	2 H83592	hypothetical prote
11	302	11.2	557	2 A25493	tryptophan 2-mono
12	288	10.7	520	2 JH0817	amine oxidase (fla
13	287.5	10.6	723	1 S30105	tryptophan 2-mono
14	285.5	10.6	500	2 T03387	polyamine oxidase
15	283	10.5	527	2 A36175	amine oxidase (fla
16	283	10.5	556	1 A53376	tryptophan 2-mono
17	271	10.0	520	2 A31870	amine oxidase (fla
18	270.5	10.0	526	2 J70528	amine oxidase (fla
19	269	10.0	471	2 S78290	hypothetical prote
20	267.5	9.9	1265	2 F71429	hypothetical prote
21	265.5	9.8	755	2 A13228	tryptophan 2-mono
22	259	9.6	755	1 DAAGWT	tryptophan 2-mono
23	256	9.5	499	2 I51346	monoamine oxidase
24	252.5	9.3	527	2 S03974	amine oxidase (fla
25	251	9.3	755	1 Q0AG4T	tryptophan 2-mono
26	248	9.2	803	2 T24685	hypothetical prote
27	244.5	9.0	448	2 H70947	hypothetical prote
28	242.5	9.0	478	2 A47693	putrescine oxidase
29	242.5	9.0	516	2 D96682	protein F1E22.18 [

30	240.5	8.9	531	2 S28260	achacin precursor
31	231.5	8.6	483	2 T21327	hypothetical prote
32	231.5	8.6	749	2 I39708	tryptophan 2-mono
33	225.5	8.3	488	2 T47787	hypothetical prote
34	224.5	8.3	533	2 T09935	hypothetical prote
35	220.5	8.2	508	2 S54021	FMS1 protein - yea
36	216	8.0	489	2 A47259	corticosteroid-bin
37	209.5	7.8	770	2 T26783	hypothetical prote
38	205	7.6	490	2 A84861	probable amine oxi
39	198.5	7.3	527	2 T33175	hypothetical prote
40	198.5	7.3	1000	2 T39423	hypothetical prote
41	186	6.9	495	2 S5273	amine oxidase (fla
42	186	6.9	536	2 T34218	hypothetical prote
43	184	6.8	566	2 F1403	hypothetical prote
44	184	6.8	570	2 A39597	phytoene dehydroge
45	183.5	6.8	474	2 S16250	phytoene dehydroge

ALIGNMENTS

RESULT 1

JE0266  
L-amino-acid oxidase (EC 1.4.3.2) - eastern diamondback rattlesnake  
N:Alternate names: LAAO; ophio-amino-acid oxidase  
C:Species: Crotalus adamanteus (eastern diamondback rattlesnake)  
C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: JE0266

R:Arabekas, A.A.; Massey, V. . .  
Biochem. Biophys. Res. Commun. 248, 476-478, 1998  
A:Title: Primary structure of the snake venom L-amino acid oxidase shows high homology .  
A:Reference number: JE0266; MUID:98369573; PMID:9703950  
A:Accession: JE0266  
A:Molecule type: mRNA  
A:Residues: 1-516 <RAI>  
A:Cross-references: UNIPROT:O93364; GB:AF071564; NID:g3426323; PIDN:AAC32267.1; PID:g3426323  
C:Keywords: oxidoreductase

Query Match 39.2%; Score 1059.5; DB 2; Length 516;  
Best Local Similarity 44.0%; Pred. No. 1.1e-60;  
Matches 218; Conservative 94; Mismatches 171; Indels 13; Gaps 7;

QY	33	LADLCEDKDYDTLLQTLNGLPHINTSHHVVIVGAGMAGLTAAKLQDAGHTVTILEAND 92
DB	25	LEECFRETDEEFLIAKNGLTATSNPKRVIVGAGMAGLSAAVYLAGHQVTVLEASE 84
QY	93	RVGGRVTRYNEKEGWYAEMGAMRIPSSHRIVQWPFVKLGVMNEFVMTDDTFFLVNGV 152
DB	85	RVGGRVTRYR--KKDWYANLGPMLPTKHRIVREYIKKFDLKLNEFSEENENAWYFIKNI 142
QY	153	RERTVVOENPDVLKYNVSESEKGISADLLDRALQKVEEVEANGCKAALEKYDRYSVK 212
DB	143	RKRREVKNPGLLEYPVKPSEEGKSAQLYVESLRKVVEELRSTNCKYLDKYDTYSTK 202
QY	213	EYLKEEGLSPGAVRMIGDLLNEQSLMVTALSEMIYDQADVNDSTVYTHEVTGCSLLPEA 272
DB	203	EYLLKEGNSPGAVDMIGDLLNEDSGYVVSPTIESLKHDDIFGYEKRFPEIVGGMQLPTS 262
QY	273	FLSVL--DVPILLNSKVHIRQSDKGVIVSYQT-QNESLMDLSADIVLVTTTAKAAPFI 329
DB	263	MVEAIKEKVQVHFARVIEIQNDREATVTYQTSANEMS--SVTADYVIVCTTSRAARI 320
QY	330	DFDPLSLSKWEALRSVHYDSSTKILLTFROKFWEDDGIKGGKSTIDGPSRVIVYPSHSF 389
DB	331	KFEPPLPKKAHALRSVHYRSGTKIFLTCTKFWEDDGIHGGKSTIDGPSRVIVYPSHSF 380
QY	390	HTNETIYGLLASVYTWSDSLLFLGASDEELKALRLAKIH---GEQVWDKCTGVIVKK 446
DB	381	TSG--VGVIIA-YGIGDDANFQALDFKDCADIVINDLSLHELKPEKDIQTCHFSMIOR 437
QY	447	WSADPYSLGAFALFTPYQHLEYAQELFSSEGRVHFAGEHTAPPHAWITSMKSAIRAAVN 506
DB	438	WSLDKYANGGITTTPTFYQHFSEALTAPFKRIYFAGEYTAQFHGWIDSTIKSLGTAARD 497



A:Reference number: JC8062; PMID: 14769868  
A:Accession: JC8062  
A:Molecule type: DNA  
A:Residues: 1-701 <ARI>  
A:Cross-references: DDBJ:AB085623  
A:Experimental source: (Strain X-119-6)  
C:Comment: This enzyme precursor is a protein of 150K with hexamer structure alpha2-beta2  
ne non-covalently bound FAD as a cofactor. It catalyzes the oxidative deamination of an  
in quantitative assaying of L-glutamate existing in food and in a fermentation process.  
C:Genetics:  
A:Gene: Lgox  
A:Start codon: GTG  
C:Keywords: hexamer structure; L-glutamate oxidase

Query Match 23.7%; Score 641; DB 2; Length 701;  
Best Local Similarity 27.2%; Pred. No. 1.8e-33;  
Matches 170; Conservative 95; Mismatches 195; Indels 164; Gaps 14;  
  
QY 49 LQGLPHINTSHHVVIVGAGMAGLTAALKLQDAGHTVTILEAN-DRVGRVETYNKEK-- 105  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
48 IDGNLPPGPPKRLILVAGIAGLVAGDILLTRAGHDVTILEANARVGGRIKTFHAKKGE 107  
QY 106 -----EGWYAGMAMRIPSSHRIVQWFKVLGVEMNEFVMTDDN-----TFY 147  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
108 PSFADPAQYAGAMRLFSFPLTLALIDKLKRLFFNFVDIDPQGNQADAPVPVPY 167  
QY 148 -----LVNGV-----RERTYVQENPDVLK-----YNVSESEK 176  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
168 KSFQDKGKTWNGAPSEPKPEKPNHRTWRTNREQVRRQAQYATDPSSINEGFHLGCETR 227  
QY 177 ISADLLDRALOKVKEVEAN-----GCKAALEKDYRSVKEYLKEEGG 220  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
228 LTVSDMVNQALFVRDYSVKQDDGTRVKNPKFEMLAGWADVVRDFDGYSMGRFLREYAE 287  
QY 221 LSPGAVRMIGDLNQGSLMYTALSEMIYQADVNSVTYHETGSDLLPEAFSLVDLP 280  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
288 FDEAVEAIGTIENNTSRJHLAFTHSFLGRSDIDPRATYWEIEGSRMLPETLAKDLRDQ 347  
QY 281 ILLNSKVKHROSCK-----QVIVSYQTGNE-----SSLMDLSADIVLVTTTA 323  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
348 IVMQRMVRLYYDFCRDGHGELTGPCGPAVAIQVPEGEFYAATQTWGLAIVTIPF 407  
QY 324 KAALFIDPPDPLSISKMEALRSVHVDSSTKILLTRDRKFW----- 363  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
408 SSLRFVKVTPPFSYKRRRAVIETHYDQATKVLLEFSRRWFEADWKRELDIAIAPGLYD 467  
QY 364 -----EDD-----GIR--- 369  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
469 YYQQNGEDDAEALALPQSVNRLPTGLLGAHPSVDESRIGEQVEYRNSELRGVVRPAT 527  
QY 370 ---GGKSITDGPSTYYPSPHSFHTNETIGVLLASVTWSDLSLLFLGASDEELKELALRD 426  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
528 NAYGGSTTDNPNRPMYFESHVPQTQG-GVVLAYSWSDDAARWDSFPDABRYGVALEN 586  
QY 427 LAKIHGEQWMDKCTGV-IVKWSADPYSIGAFALTPYQHLEYAQELFSSEGRVHFAGEH 485  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
587 LQSVHGRRIEVTGAGQTQSLRDPYACCEAAVYTPHQTAFHLDDVVRPEGVYFAGEH 646  
QY 486 TAPPHAWIETSMKSAIRAATNINK 509  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
647 VSLKHAWIEGAVETAVRAIAVNE 670

RESULT 5  
A:Reference number: A75581  
A:Accession: A75581  
A:Molecule type: DNA  
A:Residues: 1-426 <KUR>  
A:Cross-references: UNIPROT:Q8YKX9; GB:BA000020; PIDN:BA078253.1; PID:g17135707; GSPDB:1  
; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; PMID:20036896; PMID:10567266  
A:Accession: A75581  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-526 <WHI>  
A:Cross-references: UNIPROT:Q9RYN6; GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF124  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DRA0274  
A:Map position: 2

Query Match 15.2%; Score 412; DB 2; Length 526;  
Best Local Similarity 27.5%; Pred. No. 6.7e-19;  
Matches 140; Conservative 86; Mismatches 194; Indels 90; Gaps 18;  
  
QY 62 VVVGAGMAGLTAALKLQDAGHTVTILEANDRVGRVETYNKEK----- 106  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
51 VLLGGGLAGASAYEMQKAGYDVQILFENGRAGORCHWTIRGGDEYTELGGFKQTCFDR 110  
QY 107 GWYAEAGMAMRIPSSHRIVQWFKVLGVEMNEFVMTDDNTFYLVNG-----VRE---R 155  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
111 GLYINPGWPWIPCHHHAVLHVAREFGVKLEPPFIMENMNAYIHREGKNGQOPTVRVQAEAR 170  
QY 156 TYVQENPDVLKYNVSES--EKGISADLLDRALOKVKEVEPANGCKAALEKDYDY---- 209  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
171 TDMQGHVAELLNKAASQGNLDTGLTTED-----KEKLLEALHEWG---FLNKDGRYVKSL 222  
QY 210 ---SVKEYLKEEGG-LSPGA-VRMIG-DLLANEQSLMYTALSEMIYQADVNSVTYH--- 260  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
223 ETSITRPGVDRDPGARLEPFTSQPIGLDILLRRLW-----SDLNQGMVYEFRS 271  
QY 261 ---EVTGSDLLPEAFSLVDLPVILLNSKVKHROSQKGVIVSYQTGNESSLMDLSADIV 317  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
272 TMFEPEVGMDAMARAFESRVRGFIKYRARVTEIKDQTDKVTATY-VDADGTTKTASGDYC 330  
QY 318 LVTTTAKAALFIDPPDPLSISKM-----BALRSVHYDSSTKILLTRDRKFEW-D 365  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
331 ICTI-----PLSILSQIKLTGVDKDLAEAIKKVPYASSFKAGVOYKRRFWEOD 378  
QY 366 DGIRGKSITDGPSTYYPSPHSFHTNETIGVLLASVTWSDLSLLFLGASDEELKELALR 425  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
379 DDYIGGISYTDLPNQLISYPNNYPTQK-GVVLGAYMFGTDVAVNWSGNSPBLRKKVVE 437  
QY 426 DLAKIHGEQWMDKCTGVIVKWSADPYSIGAFALTPYQHLEYAQELFSSEGRVHFAGEH 485  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
438 YNAQLHPAAAKEFDNGVTV-GWHRVPWTLCGYGLYNADTRERYYPYTLCARHGRMLAGEH 496  
QY 486 TAPPHAWIETSMKSAIRAATNINKVNEES 515  
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
497 TSYNWMQEGALLAATTAQVEMHKFPASSQA 526

RESULT 6  
A12498  
L-amino acid oxidase [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: A12498  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; PMID:21595285; PMID:11759840  
A:Accession: A12498  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-426 <KUR>  
A:Cross-references: UNIPROT:Q8YKX9; GB:BA000020; PIDN:BA078253.1; PID:g17135707; GSPDB:1  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr7169



Db 292 VGGMDMIGKAFQVGEGLTYTNAKVSIAQDDKGVVVYADTVTGKVTAKGD--MCVCT 349  
Qy 323 AKAAALFIDPDPPLSISKMEALRSVHYDSSTKILLTRDFKFW-EDDGIRGGKSIDTGPSRY 381  
Db 350 IPLGILQWDLAVTDEMMAIKAVPVSQGVKGLNRRFWEDEDDIYGGHSFTDQIEGL 409  
Qy 382 IYPSHSFHTNETIGVLLASYTWSDESLFLGASDEELKELALRDLAKIHGQVMDKC-T 440  
Db 410 ISYPNNLF-QDGPVLLGAFARDLGFRLAGWTPEORIEVALAQGSVHPKSYRKEPRT 468  
Qy 441 GVIVKWSADPYSGLGAFALFTPYQHLEYAQELFSSEGRVHFAGEHTAFPHAMTSMKSA 500  
Db 469 GASV-AWSRVPWTLGCCARWNEETRKHQYQTLVAMDRIRVLAGEHASVYVGCWMEGALLSS 527  
Qy 501 IRAAYTNINKVA 511  
Db 528 LDAITRLHKRA 538

RESULT 9  
G87384  
amine oxidase, flavin-containing [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: G87384  
R:Nierman, W.C.; Feldbiyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: G87384  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-534 <STO>  
A:Cross-references: UNIPROT:Q9A9A3; GB:AE005673; NID:G13422395; PIDN:AAK23075.1; GSPDB:G  
C:Genetics:  
A:Gene: CC1091

Query Match 13.1%; Score 353.5; DB 2; Length 534;  
Best Local Similarity 27.8%; Pred. No. 46-15;  
Matches 141; Conservative 64; Mismatches 226; Indels 77; Gaps 17;

Qy 48 TLDNGLPHINTSHHYVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETRYNE--- 104  
Db 51 TLTGAK--NTK--VILGAGLAGTAAAYEMSKAGTQVQVILEARDYAGRCOTARKGFH 106  
Qy 105 -----KEGWYAEIMGAMRIPSSHRIYQWFKVLGVEMNBFVMTDNTF--YLNG 151  
Db 107 TDLNGTQVCEPDDGHYINHGAWRIPYHRSSTLHYTKSFGVLLESFVNDNDASYVYFEK 166  
Qy 152 VRERTYVQENPDVLKYNVSESEKISADLLDRALQKVEVEANGCKAALEKYDRYSV 211  
Db 167 -----KGP-----LNGKPYRKEIAADVRYGTAEIVAKAASAGALDAPLSGVDRERF 213  
Qy 212 KEYLKEEGLS-----PGAVRMIG-----DLLNEQSLMYTAL 243  
Db 214 VAYLVNEGRLSKDLTYKGTGEGRGSVHPGAGNPGPKELEPPFAFKDVLDSNA--WRVL 271  
Qy 244 SEMI-YDQADVNDVSYTTEVTGSDLLPEAFSLVDLPILNLSKVHQRQSDKGVISYQ 302  
Db 272 SSVTGYEQ-----QRTMLQPIGGMDQIAKAFKRVAPMIRYSTVVQIKQSPGTGVTSFK 326  
Qy 303 TGNESLMDLSADIVLVTTAKAALFIDPDPPLSISKMEALRSVHYDSSTKILLTRDFK 362  
Db 327 -GPDGKGEVTADYCVCTIPLSVLQIDLD--ASAPFKAAMEGVAYAPVNIKGLQMKSRF 383  
Qy 363 WED-DGIRGGKSIDT-GPSRYIYPSHSFHTNETIGVLLASYTWSDESLFLGASDEELK 420  
Db 384 WEDRHHIYGGHIYTLAGIGSISLPSYQWQAK--GVLIGYAFGEAAARSAPADRA 441  
Qy 421 ELALRDLAKIHGEQWMDKCTGVIVKWSADPYSGLGAFALFTPYQHLEYAQELFSSEGRVH 480

Db 442 AFPAVAGGQKVFPEYA-ENFENAFPSFWHLAEHLNLCGWAEBNGRKEAYPIILCEPDGRLY 500  
Qy 481 PAGEHTAFPHAMTSMKSAIRAATNIN 508  
Db 501 LAGEHLSYLGGWQAGAISSAMQOIAKIH 528

RESULT 10  
H83592  
hypothetical protein PA0421 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: H83592  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: H83592  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-496 <STO>  
A:Cross-references: UNIPROT:Q9I692; GB:AE004479; GB:AE004091; NID:G9946272; PIDN:AAG0381  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA0421

Query Match 11.4%; Score 307; DB 2; Length 496;  
Best Local Similarity 27.0%; Pred. No. 3-6e-12;  
Matches 129; Conservative 83; Mismatches 200; Indels 66; Gaps 20;

Qy 63 VIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETRYNEKEGWYAEIMGAMRI-PSH 121  
Db 31 IVWGAGLAGLGAAYELQDQGWQVTVLEARPQVGGRSGLATSE---W---VGNQKVOPTLN 84  
Qy 122 RIVQWFKVLGVEMNEFVMTDNTFYLNVGRERTYVYVQENPDVLKYNVSE---SEKGS 178  
Db 85 AYLDTF-KLKPVPAPDFVTRPS---YLIDG-----LYYSSDDLALQPNVA 126  
Qy 179 AD-----DLLDRALQKVEVEANGCKAALEKYDRYSVKYKLEGGLSPGAVRMIG 230  
Db 127 ADLKRFEFTLDDLSASISDPLNPASSN---TLFALDQWNAARWL-DKLNLSPTARLLVN 181  
Qy 231 DLLNEQ-----SLMYTALSEMIYDQADVNDVSYTTEVTGSDLLPEAFSLVDLPILL 283  
Db 182 QRIRSRVDEPSRLSLLLAQQGRAYRGVDDHD-LRAARLPGGSQVLAFAFKQIKT-IKT 239  
Qy 284 NSKVHQRQSDKGVISYOTGNESLMDLSADIVLVTTTAKAALFIDPDPPLSISKMEAL 343  
Db 240 KSKVSSIVQAKGVAV--KAGSET-----YKADYVVVLAIVPLKALGOIQMTPSLSGTQMSAL 293  
Qy 344 RSVHYDSSTKILLTRDFKFWEDDGIRGKSIDTGPSRYIY-PSHSFHTNETIGVLLASY 402  
Db 294 KGTNYGWRDQILLKFKRPVWDDKSRLSGEIPESDQGLGMIWVEPALKGCANVLINLS---- 349  
Qy 403 TWSDESLFLGASDEELKELALRDLAKIHGQVMDKCTGVIVKWSADPYSGLGAFALFTP 462  
Db 350 --GDNARVLQAFGRQWVDQVLIRMNKFY-PKMRGAFAGYAIRRYSDPFGTGGSYLAYGP 406  
Qy 463 YQHLEYAQELFSSEGRVHFAGEHT-APPHAMTSMKSAIRAATNINKV-ANEESTIE 518  
Db 407 QQVTRFRWIRWEOPLSRVAFAGEHTDALYPGTIEGALRSRGAASQVRDLIYAGKTPIVIE 464

RESULT 11  
A25493  
tryptophan 2-monoxygenase (EC 1.13.12.3) - Pseudomonas syringae pv. savastanoi  
C:Species: Pseudomonas syringae pv. savastanoi  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A25493  
R:Yamada, T.; Palm, C.J.; Brooke, B.; Kousge, T.





